us-09-997-428-408.rag

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Human BRO
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 Ada17936
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ABU865314
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ABR89863
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ABR9968863
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ADE26396
AAW7866
AAM20693
AAW6206
AAY4456
AAY872834
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ABU88774
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ADC57888
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                                                                                                       5, 2004, 14:09:33; Search time 54 Seconds (without alignments) 544.166 Million cell updates/sec
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                                                                                                                                                                    US-09-997-428-408
502
1 MKLAALLGLCVALSCSSAAA......QAVGAVKALKALLGALTVFG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                          1586107 segs, 282547505 residues
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                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
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Listing first 100 summaries
                                                                               OM protein ~ protein search, using sw model
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AAX46488
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AAB65280
ABB059173
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ABU829020404
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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9805-008994179-9805-00899448P-9805-00899448P-9805-00899448P-9805-00899448P-9805-00990552P-9805-00990552P-9805-00990453P-9805-00990445P-9805-00990445P-9805-00990645P-9805-00990645P-9805-00990645P-9805-00990645P-9805-00990645P-9805-00990645P-9805-00990645P-9805-00990645P-9805-009906445P-9805-009906445P-9805-009906445P-9805-009906445P-9805-009906445P-9805-009906445P-9805-009906445P-9805-009906445P-9805-009906445P-9805-009906445P-9805-009906445P-9805-009906445P-9805-009906445P-9805-009906445P-9805-009906445P-9805-00990645P-9805-00990645P-9805-0096449P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-009649P-9805-0096449P-9805-0096449P-9805-0096449P-9805-0096449P-9805-0096449P-9805-0096449P-9805-0096449P-9805-0096449P-9805-0096449P-9805-0096449P-9805-0096449P-9805-0096449P-9805-0096449P-9805-0096449P-9805-0096449P-9805-0096449P-9805-0096444P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-00964448P-9805-0
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18-7UN-1998;
19-7UN-1998;
19-7UN-1998;
22-7UN-1998;
22-7UN-1998;
23-7UN-1998;
23-7UN-1998;
23-7UN-1998;
24-7UN-1998;
24-7UN-1998;
24-7UN-1998;
   Novel hum
Human sec
                                                                                                                                                                                                                                           Membrane-bound polypeptide, PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping.
 Abo06270 Abr59306 B
                                                         ALIGNMENTS
   ABO06270
ABR59306
                                                                                                                               AAY66757 standard; protein; 104 AA
                                                                                                                                                                                                                 Membrane-bound protein PRO1245.
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98US - 0087607P

98US - 0087627P

98US - 0088022F

98US - 0088023P

98US - 0088023P

98US - 0088023P

98US - 0088030P

98US - 00880531P

98US - 00880531P
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98US-0089653P.
98US-0089801P.
98US-0089907P.
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    99
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    31.9
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110 - 7UN - 1998
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                                                                                                                                                                                                                                                                                                                                                                           02-JUN-1999;
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    160
                                                                                                                                                           AAY66757;
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The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors. TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadheains, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful to the preparation of PRO polypeptides, especially by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lung Specific Gene; LSG; Lng107; human; diagnostic marker; prognosticate; lung cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLAALIGECVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                               Membrane-bound proteins and related nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 502; DB 3;
100.0%; Pred. No. 1.4e-48;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lung specific gene protein Lng107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY44458 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Fig 290; 822pp; English
                                                                                                                                                                                                                                                                                                            Goddard A,
98US-0096960P.
98US-0097022P.
98US-0097141P.
98US-0097661P.
98US-0097952P.
98US-0097952P.
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98US-0098525P.
98US-0100634P.
99US-0115565P.
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Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant techniques
                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-072883/06.
                                                                                                                                                                                                                                                                                                            Chen J,
Yuan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAZ65103
                                                                       26-AUG-1998;
26-AUG-1998;
26-AUG-1998;
26-AUG-1998;
26-AUG-1998;
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The present sequence is a lung specific gene (LSG) protein Ingl07 from human clone ID 586271. The LSG has high level of tissue specificity for lungs and is overexpressed in cancercous tissues. The sequence serves as a diagnostic marker for detecting, monitoring, staging and prognosticating lung cancer. The diagnosis involves comparing levels of LSG in samples obtained from patient and normal control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease, anticancer; anti-inflammatory; antimicrobial, nocropic, neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psordiasis; parquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Althelmer's disease; schizophrenia; parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAABAGAGTLANPLGTLNPLKLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTINPLKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                  A new method for diagnosing, monitoring and staging lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human signal peptide containing protein HSPP-65 SEQ ID NO:65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 100.0%; Score 502; DB 3; Length 104; Local Similarity 100.0%; Pred. No. 1.4e-48; nes 104; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 38-39; 40pp; English
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                                                                                                    99WO-US010344
                                                                                                                                  98US-0086212P
                                                                                                                                                                                              Sun Y;
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                                                                                                                                                               (DIAD-) DIADEXUS LLC
                                                                                                                                                                                                 Macina RA,
                                                                                                                                                                                                                           WPI; 2000-116320/10
N-PSDB; AAZ29723.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 104 AA;
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                                                               25-NOV-1999.
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                                                                                                    12-MAY-1999;
                                                                                                                                   21-MAY-1998;
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                Homo sapiens.
                                           WO9960160-A1
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1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Score 502; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PRO1245 (UNQ629) protein sequence SEQ ID NO:408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB65280 standard; protein; 104
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                                                                                  WPI; 2000-160673/14.
N-PSDB; AAZ98173.
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 104 AA;
                                                 Lal P, Tang YT,
Akerblom IE, Au
Bandman O;
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                11-DEC-1998;
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(GETH ) GENENTECH INC.
                                WO200073454-A1
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24-FEB-2000;
02-MAR-2000;
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16-DEC-1999;
20-DEC-1999;
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06-JAN-2000;
11-FEB-2000;
Homo sapiens.
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                                                                                                                                                                                                                             28-JUL-1999
17-AUG-1999
controlled to Adapasaye encome Adailor 10 Adailor) winton represent time human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have carticancer, anti-inflammatory, anti-inflammatory, anti-inflammatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, cartiviosis, psoriasis, acquired immune deficiency syndrome, ansemia, asthma, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's Parkinson's or Huntington's cirrobase, psoriasis, acquired immune deficiency syndrome, ansemia, congestive or deseases, activity or unclaic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diseases, and monitoring), in gene therapy, as antisense, triplex-forming or ribozyme therapeutics (Ab) and to screen for agoinsts and antegonists or specific antibodies (Ab) and to screen for agoinsts and antegonists, in constituted diseases (in usual immunoassays), as therapeutic antagonists, in competitive drug screens, and for purification of HSPP from natural
                                                                                                                                                                                                                               New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease.
                                                                                                     TT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR; Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                            to AAZ98242 encode AAY87224 to AAY87357 which represent
                                                                                                                                                                                                                                                                                                          Claim 1; Page 206; 327pp; English.
 98US-0094983P.
98US-0102686P.
98US-0112129P.
                                                                          (INCY-) INCYTE PHARM INC
   31-JUL-1998;
01-OCT-1998;
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2000WO-US005004. 2000WO-US005841. 2000WO-US006884.

2000WO-US004414

99US-0141037P. 99US-0143048P. 99US-0144758P. 99US-0145698P. 99US-0146222P.

2000WO-US008439

99WO-US021090 99US-0158663P

99WO-US028313 99WO-US028301 99WO-US030095 99WO-US030911

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The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bloactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO mucleotide sequences, and their fragments, can be used as hybridisation probes, in biromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO mucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF4470 represent PCR primers and hybridisation probes used in the lisolation of human PRO sequences. AAP44487 to AAP44470 to AAP645300 represent human PRO sequences and protein sequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                         PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                              Godowski P
Paoni NF;
Wood WI;
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Asnkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Perrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Fig 290; 935pp; English.
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les 104; Conservative
                                                                                                                                                                                                                                                              WPI; 2001-032160/04.
                                                                                                                                                                                                                                                                                                  N-PSDB; AAF44249.
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1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL

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Indels

ö DB 5;

Length 104;

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RESULT 5 AAU86141

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1 MKLAALIGICVALSCSSAAAFIVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
                                                                                                                                                                                                                                                                                                                                                                                Human, PRO, cytostatic, tumour, cancer, breast, lung, stomach, liver,
horse, cow, dog, cat, sheep, pig, goat, rabbit, ADEPT,
antibody-dependent enzyme mediated prodrug therapy.
                                                                                      1 MKLAALLGLCVALSCSSAAAPLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
                                                                                                                                                                      LSSLGIPVNHLIEGSQKCVABLGPQAVGAVKALKALLGALTVFG 104
                                                                                                                                                  LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
                          100.0%; Score 502; DB 5;
100.0%; Pred. No. 1.4e-48;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                            ABU58095 standard; protein; 104 AA
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97US-0062250P.
97US-0065186P.
97US-006311P.
97US-0066770P.
98US-0078910P.
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98US-0084600P.
98US-0087106P.
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9805-00876079
9805-00876219
9805-00880219
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9805-00880289
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                                                                                                                                                                                                                                                                                                                                                    Human PRO polypeptide #127
                                                                                                                                                                                                                                                                                                                       14-APR-2003 (first entry)
                           Query Match
Best Local Similarity 100.0
Matches 104; Conservative
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   Sequence 104 AA;
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11-JUN-1998;
11-JUN-1998;
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07-MAY-1998;
28-MAY-1998;
02-JUN-1998;
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25-FEB-1998;
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12-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of novel human PRO polypeptides and the polynuclectide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polymucleotide sequences are also useful in gene therapy. AAU86122 PAU86162 represent the human PRO polypeptides of the invention
                                                                                                                                                                                                                                                           Human, PRO, benign tumour; malignant tumour; lymphoid malignancy,
leukaemia, neuronal disorder; stromal disorder; blastocoelic disorder;
inflammatory disorder; immune disorder; anglogenic disorder; cytostatic;
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1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thirty five nucleic acids encoding PRO polypeptides, useful for benign or malignant tumors, leukemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hillan KJ;
Stone DM;
                                  61 LSSLGIPVNHLIEGSOKCVAELGPQAVGAVKALKALLGALTVFG 104
                                                  61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
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Smith V,
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Pitti RM, Roy MA,
                                                                                                                                         AAU86141 standard, protein; 104 AA
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99US-0133459P.
99US-0140650P.
99US-0140653P.
99US-0144758P.
99US-014622P.
99US-0149395P.
99US-0149395P.
99US-0149395P.
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99WO-US028301.
99WO-US028634.
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                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                 Human PRO1245 polypeptide.
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Wood WI;
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N-PSDB; ABK40267.
                                                                                                                                                                                                                                                                                                            neuroprotective
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Watanabe CK,
                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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11-MAY-1999;
02-JUN-1999;
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22-JUN-1999;
20-JUL-1999;
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28-JUL-1999;
17-AUG-1999;
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18-AUG-1998 18-AUG-1998 18-AUG-1998 18-AUG-1998 18-AUG-1998 26-AUG-1998 27-AUG-1999 27-AUG-1999 28-AUG-1999 28-AU DB 6; Length 104;

100.0%; Score 502;

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2000WO-US023328 2000US-0230978P

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WPI; 2003-247083/24.
N-PSDB; ABX80385.
                                                                                                                                                                    16-SEP-1998;
17-SEP-1998;
07-0CT-1998;
08-MAR-1999;
08-MAR-1999;
15-SEP-1999;
15-SEP-1999;
15-SEP-1999;
16-DEC-1999;
10-DEC-1999;
10-DEC-1999;
10-DEC-1999;
11-FEB-2000;
22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
10-MAR-2000;
11-MAR-2000;
11-MAR-2000;
11-MAR-2000;
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17-MAY-2000;
22-MAY-2000;
30-MAY-2000;
02-JUN-2000;
28-JUL-2000;
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20-MAR-2000;
30-MAR-2000;
       11-70N-1998
11-70N-1998
11-70N-1998
12-70N-1998
16-70N-1998
16-70N-1998
16-70N-1998
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18-JUN-1998;
18-JUN-1998;
18-JUN-1998;
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                                                                                                                       17-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang Z;
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                                                                                                                                                                                                       Human; PRO; hypertrophy of neonatal heart; anglogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; retinal reurons cell growth inhibitor; T-lymphocytes erimulation; retinal heurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; dermanial and disorder; cell factoris pigmentosum; kidney disorder; dermanial cell proliferation; Berger disease; dermatitis, herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis.
                                          1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLKLL
                            1. MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
           0; Gaps
                                                               61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
Best Local Similarity 100.0%; Pred. No. 1.4e-48; Matches 104; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                         Novel human secreted or transmembrane protein PRO1245.
                                                                                                                                  ABUS9173 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                         9713-0049787P.
9713-0062280P.
9713-0062280P.
9713-0065111P.
9813-0065711P.
9813-0065711P.
9813-0083122P.
9813-008719P.
9813-008719P.
9813-008719P.
9813-008719P.
9813-008719P.
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9813-0088127P.
9813-0088128P.
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98US-0088742P.
98US-0088810P.
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                                                                                                                                                                        28-APR-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                          16-JUN-1997;
17-OCT-1997;
12-NOV-1997;
13-NOV-1997;
24-NOV-1997;
24-NOV-1998;
26-FEB-1998;
26-APR-1998;
28-APR-1998;
28-APR-1998;
02-JUN-1998;
02-JUN-1998;
04-JUN-1998;
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05-JUN-1998;
05-JUN-1998;
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10-JUN-1998;
10-JUN-1998;
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                                                                                                                RESULT
                                                                                                                          ABU591
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13-FEB-2003

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The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bloactive modecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus cuseful for treating cardiac insufficiency disorders. PRO1364 and PRO1366 stimulate adrenal cortical capillary endothelial growth, and PRO1366, PRO943, PRO928, PRO926, PRO1068 or PRO535, PRO926, PRO943, PRO926, PRO1068 or PRO535, PRO926, PRO941 are thus conditions or disorders where angiogeneats would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating conclusions timulated proliferation of endothelial growth factor (VEGP) stimulated proliferation of endothelial growth factor (VEGP) stimulated proliferation of stimulate proliferation of remune response. PRO826, PRO1368 and PRO1375 stimulate proliferation of stimulate proliferation of stimulate proliferation of companies. PRO828, PRO926, PRO1068 or PRO1132 enhance survival of retinal neurons cells (PRO3132 stimulate proliferation of descreased mesangial cell function of mammalian kidney insorders associated with decreased mesangial cell function such as Berger cother chemical proliferation and/or redifferentiation of chost cother compirement of the properties of cother corpused for treating spigmentosum, AMD. PRO919, PRO913 and proliferation and/or redifferentiation of chost cother corpused for treating sports influence in culture and are thus useful for treating sports injuries, and architics. This is the amino acid sequence of a novel human PRO protein
Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes the therapeutically useful for enhancing immune response and in cancer treatments.
                                                                                                                                                 Claim 12; Fig 290; 648pp; English
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9 9 1 MKLAALIGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKIL 1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL .. 100.0%; Score 502; DB 6; Length 104; 100.0%; Pred. No. 1.4e-48; ive 0; Mismatches 0; Indels 0 Best Local Similarity 100. Matches 104; Conservative Query Match ઠે

61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104 ò

ABU82685 standard; protein; 104 AA RESULT 8 ABU82685

26-JUN-2003 (first entry) ABU82685;

Human secreted/transmembrane protein PRO1245.

Human; PRO; secreted protein; transmembrane protein; cardiac insufficiency disorders; angiogenesis; wound healing; cancerous tumour; immune response; retinal disorder; sight loss; retinitis pigmentosum; age-related macular degeneration; AMD; kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis; Crohn's disease; sports injury; arthritis.

Homo sapiens.

US2003032023-A1

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97105-0049787P

9705-00622200P

9705-0062311P

9705-0065311P

9705-0065311P

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9705-0065311P

9805-0083122P

9805-0083122P

9805-0087106P

9805-0087106P

9805-0087106P

9805-0087108P

9805-0087108P

9805-008872P

9805-008972P

9805-009974P

9805-009074P

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9805-009074P
                                           14-NOV-2001; 2001US-00990711
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05-JUN-1998;
05-JUN-1998;
05-JUN-1998;
10-JUN-1998;
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PR 25-JUN-1998, 98US-0090678P, PR 25-JUN-1998, 98US-0090699P, PR 25-JUN-1998, 98US-0090695P, PR 25-JUN-1998, 98US-0090692P, PR 25-JUN-1998, 98US-0090692P, PR 25-JUN-1998, 98US-0090692P, PR 25-JUN-1998, 98US-0090692P, PR 25-JUN-1998, 98US-0091602P, PR 25-JUN-1998, 98US-0095118P, PR 25-JUN-1998, 98US-0095118P, PR 25-JUN-1998, 98US-0095612P, PR 25-JUN-1998, 98US-0095613P, PR 25-JUN-1998, 98US-0095613P,
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1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 502; DB 6; Length 104; 100.0%; Pred. No. 1.4e-48; ive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LSSLGIPVNHLIEGSOKCVAELGPAVGAVKALKALLGALTVFG 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA019895 standard; protein; 104 AA
02-JUN-1999; 99WO-US012252.
23-JUN-1999; 99US-0141037P.
20-JUL-1999; 99US-0144758P.
26-JUL-1999; 99US-0145698P.
28-JUL-1999; 99US-0145698P.
28-JUL-1999; 99US-0145698P.
17-AUG-1999; 99US-0145698P.
15-SEP-1999; 99US-0145622P.
15-SEP-1999; 99WO-US021547.
08-OCT-1999; 99WO-US021547.
01-DEC-1999; 99WO-US02180.
01-DEC-1999; 99WO-US0280301.
01-DEC-1999; 99WO-US028031.
01-DEC-1999; 99WO-US028031.
01-DEC-1999; 99WO-US028031.
01-DEC-1999; 99WO-US028031.
01-DEC-1999; 99WO-US028031.
01-DEC-1999; 99WO-US028031.
02-JUN-2000; 2000WO-US02837P.
02-JUN-2000; 2000WO-US02837P.
02-JUN-2000; 2000WO-US02837P.
02-JUN-2000; 2000WO-US02837P.
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Best Local Similarity 100.
Matches 104; Conservative
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2000WO-US014941.
2000WO-US015264.
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2001WO-US021066
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30 - MAY - 2000; 2
28 - JUL - 2000; 2
11 - AUG - 2000; 2
23 - AUG - 2000; 2
4 - AUG - 2000; 2
08 - FEB - 2001; 2
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15-SEP-1999;
16-SEP-1999;
01-DEC-1999;
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06-JAN-2000;
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06-JAN-2000;
11-FEB-2000;
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26-MAR-2000;
11-MAR-2000;
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                                                                                                                              The present invention provides the human and murine uteroglobin related protein 1 (UGRP1) promoters. The sequences can be used in the diagnosis of and prediction of prediagosition to respiratory disorders such as asthma. The present sequence is a protein sequence shown in the exemplification of the invention
                                                                                                                                                                                                                                                               1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical; diagnostic; therapeutic; gene therapy.
                                                      New human UGRP1 nucleic acid, useful for diagnosing or predicting a predisposition to develop a respiratory disorder or determining the prognosis of a subject having or suspected of having a respiratory disorder e.g., asthma.
                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                      Length 104;
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                                                                                                                                                                                                                                            0; Indels
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100.0%; Pred. No. 1.4e-48;
ative 0; Mismatches 0;
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                                                                                                               Disclosure; Page 79-80; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        ABU60604 standard; protein; 104 AA
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97US-0062180P.
97US-0065111P.
97US-0065311P.
97US-0065311P.
97US-0063312P.
98US-0084600P.
98US-008460P.
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Best Local Similarity 100.
Matches 104; Conservative
                                      WPI; 2003-184004/18.
                  Niimi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2002160384-A1.
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17-OCT-1997;
05-NOV-1997;
13-NOV-1997;
24-NOV-1997;
24-NOV-1998;
26-MAK-1998;
28-MAK-1998;
02-JUN-1998;
02-JUN-1998;
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                   Kimura S,
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ABU60604
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9705-00622507
9705-00652118
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9805-0075945P
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9805 - 0089532P
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9805 - 0089538P
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9805 - 0089598P
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98US-0089801P.
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98WO-US025108.
99WO-US000106.
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11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341
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2000WO-US006319
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 97US-0049787P
16 - JUN - 1997;

17 - OCC - 1997;

18 - OCC - 1997;

26 - FEB - 1998;

28 - ARX - 1998;

28 - ARX - 1998;

29 - JUN - 1998;

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06-JAN-2000;
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05-JAN-1999;
08-MAR-1999;
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16-SEP-1998
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 The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the mucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bloadthe molecule to a cell expressing a PRO protein and for modulating at least one bological activity of a cell. The PRO polypeptides or polymerical activity of a cell. The PRO polypeptides or polymerical activity of a cell. The PRO polypeptides or polymerical activity of a cell. The PRO polypeptides or in generating probes. The PRO polypeptides are also useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for patural sources. The sequences presented in ABUG0478-ABUG0624 are the PRO polypurcleotides of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
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                                                                     Ρ.
                                                                                                                                                                          New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                        Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
Rerrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Goddowski F
grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
Gry MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; PRO polypeptide; secreted protein; transmembrane protein;
genetic disorder; antibacterial; immunosuppressive.
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                                                                                                                                                                                                                                   Claim 12; Fig 290; 650pp; English.
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    28-AUG-2001; 2001US-00941992
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                              (GETH ) GENENTECH INC.
                                                                                                                                        WPI; 2003-288106/28.
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Matches 104; Conserv
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                                                                                                Roy MA,
Zhang Z;
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ABU13986
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virucide, hepatotropic; antiinflammatory; neuroprotective; gene therapy; PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy; cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia; lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
                                                                                                                                                           Human; secreted and transmembrane protein; cytostatic; anti-HIV;
                                                                                                                        Novel human secreted and transmembrane protein PRO1245.
                   ABU72571 standard; protein; 104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             9705-0049787P

9705-0062250P

9705-0065311P

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9805-008322P

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98US-0089532P.
98US-0089538P.
98US-008959P.
98US-0089600P.
98US-0089653P.
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                                                                                          (first entry)
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                                                                                                                                                                                                                                                       drug screening
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18-JUN-1998;
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05-JUN-1998;
05-JUN-1998;
09-JUN-1998;
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                                                       ABU72571;
The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides, for linking biological activities of cells expressing PRO polypeptides, and for linking intentifying agonists or antagonists. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in the preparation of Antisense RNA and DNA, in the perspace and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, to construct hybridisation probes for mapping the generation, as choosesement the PRO polypeptide, and for the generic analysis of individuals with genetic disorders, in gene therapy, for chromosome identification, as chromosome markers, and for generating probes for PCR, Northern analysis, Southern analysis and Western analysis. ABU14006 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at sequence gov/psipsDIBINITY.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                Godowski PJ;
Paoni NF;
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.
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Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi JC, Gurney A, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
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100.0%; Pred. No. 1.4e-48;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                  08-NOV-2000) 2000WO-US030952.
01-DEC-2000) 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
01-UTN-2001; 2001WO-US017600.
20-UTN-2001; 2001WO-US019592.
29-UTN-2001; 2001WO-US01066.
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2000WO-US015264
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Matches 104; Conservative
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N-PSDB; ABX64209.
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                                      30-MAR-2000;
15-MAY-2000;
17-MAY-2000;
22-MAY-2000;
30-MAY-2000;
28-JUN-2000;
28-JUL-2000;
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08-NOV-2000;
01-DEC-2000;
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Zhang Z;
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RESULT 12

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18-JUN-1998; 98US-0089908P.

16-SEP-1998; 98WO-US019437.

07-OCT-1998; 98WO-US019437.

07-DCT-1998; 98WO-US019437.

07-DCT-1998; 98WO-US019437.

08-JAN-1999; 99WO-US0216108.

08-MAR-1999; 99WO-US0216108.

15-SEP-1999; 99WO-US021647.

16-DEC-1999; 99WO-US021665.

16-DEC-1999; 99WO-US021665.

17-AUG-2000; 2000WO-US03128.

18-AUG-2000; 2000WO-US03128.

19-AUG-2000; 2000WO-US03128.

29-AUN-2001; 2001WO-US031665.

29-AUN-2001; 2001WO-US031665.
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28-AUG-2001; 2001US-00941992
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DL; Godowski PJ; Paoni NF; ,, Wood WI; Eaton Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,

N-PSDB; ACA64431

New genes and secreted and transmembrane polypeptides (e.g. PRO183 or PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's disease

Claim 12; Fig 290; 663pp; English.

The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATCC Deposit No. 203621, 552-pPA, 819-PPA, 209439, 203135, etc.) or a sequence with at least 80% identity to a DNA encoding a PNO polypeptide. The PNO polypeptides or polypeptide are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or ancers (e.g. ovarian cancer, colorectal cancer, Kaposis sarrooms, leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's disease in mammals. The PNO polypeptides are useful in drug screening,

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particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO gense are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
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                                                                                                                                                                                                      1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
                                                                                                                                                                                                                       1 MKLAALIGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEBGAGTLANPLGTLNPLKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; PRO; secreted; transmembrane; pharmaceutical; diagnostic;
                                                                                                                                                                             ;
0
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                                                                                                                                                100.0%; Score 502; DB 6; Length 104; 100.0%; Pred. No. 1.4e-48; cive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                           LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
                                                                                                                                                                                                                                                                          LSSLGI PVNHLIEGSOKCVAELGPOAVGAVKALKALLGALTVFG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted/transmembrane protein, #163.
                                                                                                                                                                                                                                                                                                                                                       ABU59320 standard, protein; 104 AA.
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970S-0062250P.
970S-0065211P.
970S-0065311P.
980S-0006770P.
980S-008322P.
980S-0087607P.
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980S-0087607P.
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                                                                                                                                                                             Matches 104; Conservative
                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                          Sequence 104 AA;
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17-OCT-1997;
12-NOV-1997;
13-NOV-1997;
24-NOV-1997;
24-PEB-1998;
20-MAR-1998;
28-MAY-1998;
02-JUN-1998;
02-JUN-1998;
02-JUN-1998;
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05-JUN-1998;
05-JUN-1998;
05-JUN-1998;
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5-UW-1998 0-UW-1998 0-UW-1998 0-UW-1998 0-UW-1998 1-UW-1998 1-UW-1998 1-UW-1998 1-UW-1998 5-UW-1998 5-UW-1998 7-UW-1998	17UN 1998; 18UN 1998; 18UN 1998; 19UN 1998; 19UN 1998; 19UN 1998; 22UN 1998; 22UN 1998; 24UN 1998; 24UN 1998; 24UN 1998; 24UN 1998; 24UN 1998; 24UN 1998; 25UN 1998; 26UN 1998; 26UN 1998; 27UN 1998; 27UN 1998; 27UN 1998; 28UN 1998; 28UN 1998; 28UN 1998; 28UN 1998;	1.10L-1994 2.70L-1998 2.70L-1998 2.70L-1998 2.70L-1998 2.70L-1998 3.70L-1998 3.70L-1998 3.70L-1998 3.70L-1998 3.70L-1998 3.70L-1998 4.40G-1998 4.40G-1998 4.40G-1998 4.40G-1998
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PR 10-AUG-1998 98US-0095929P.
PR 11-AUG-1998 98US-0096146P.
PR 11-AUG-1998 98US-0096176P.
PR 11-AUG-1998 98US-0096176P.
PR 11-AUG-1998 98US-0096176P.
PR 11-AUG-1998 98US-0096176P.
PR 11-AUG-1998 98US-0096171P.
PR 26-AUG-1998 98US-0097171P.
PR 26-AUG-1998 98US-0109717P.
PR 26-AUG-1999 99US-0160193 98US-0160193 PR 26-AUG-1999 99US-0160193 PR 26-AUG-1

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(GETH ) GENENTECH INC.
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N-PSDB; ACD44399.
10 - JUN - 1998 | 10 - JUN - 1998 | 11 - JUN - 1998 | 12 - JUN - 1998 | 12 - JUN - 1998 | 12 - JUN - 1998 | 13 - JUN - 1998 | 14 - JUN - 1998 | 17 - JUN - 1998 | 18 - JUN - 1999 | 18 - JUN - 1
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Zhang Z;
 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
                                                                                                                                                                                            MKLAALIGLCVALSCSSAAAFIVGSAKPVAQPVAALESAAEAGAGTIANPLGTLNPLKLL 60
                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, PRO polypeptide, secreted protein; transmembrane protein; genetic disorder; antibacterial; immunosuppressive.
                                                                                                                  Length 104;
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                                                                                                                                                                                                                                                   0; Indels
                                                                                                               Query Match
100.0%; Score 502; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0;
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   30-MAY-2000, 2000WG-US014941.
02-UTW-2000; 2000WG-US015264.
23-UTW-2000; 2000WG-0211637P.
28-UTL-2000; 2000WG-US020710.
11-AUG-2000; 2000WG-US02231.
23-AUG-2000; 2000WG-US023522.
24-AUG-2000; 2000WG-US023328.
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9805-0066710P
9805-0083122P
9805-0083122P
9805-0087607P
9805-0087607P
9805-0087607P
9805-0087607P
9805-0087609P
9805-0088028P
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97US-0062250P.
97WO-US020069.
97US-0065186P.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Human PRO1245 polypeptide
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17-OCT-1997;
05-NOV-1997;
12-NOV-1997;
13-NOV-1997;
25-FEB-1998;
20-MAR-1998;
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07 - MAY - 1998

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04 - JUN - 1998
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05-JUN-1998;
05-JUN-1998;
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ABO26017
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PR 11-UN-1999) 9818-0088624P.
PR 11-UN-1999) 9818-0088624P.
PR 11-UN-1999) 9818-0088624P.
PR 11-UN-1999) 9818-0088624P.
PR 11-UN-1999) 9818-0088634P.
PR 11-UN-1999) 9818-0089634P.
PR 11-UN-1999) 9818-0089634P.
PR 11-PR 11-
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us-09-997-428-408.rag

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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for modulating clentifying agonists or antagonists. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, to construct hybridisation probes for mapping the construct hybridisation probes for mapping the individuals with genetic disorders, in gene therapy, for chromosome identification, as chromosome markers, and for generating probes for PRO Northern analysis and Western analysis and Western analysis. ABO25031 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDDDILTY.html
                                                                                                                                                                                                                                                                                                                                                                                             1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKUL 60
                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKLAALIGICVALSCSSAAAFIVGSAKPVAQPVAALESAABAGAGTLANPLGTLNPLKLL 60
          Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, PRO; secreted; transmembrane; signal peptide; pharmaceutical;
diagnostic; biosensor; bioreactor; tumour; therapeutic; colon cancer;
lung cancer; breast cancer; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 502; DB 6; Length 104; Best Local Similarity 100.0%; Fred. No. 1.4e-48; Matches 104; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU59026 standard, protein, 104 AA
                                                          Claim 12; Fig 290; 661pp; English.
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97US-0062250P
97US-0065186P.
97US-0065311P.
97US-0065311P.
98US-0075945P.
98US-0078910P.
98US-008910P.
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                                                                                                                                                                                                                                                                                                                     Sequence 104 AA;
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05-NOV-1997;
12-NOV-1997;
13-NOV-1997;
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98US-0088212P.
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99WO-US028313.
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98WO-US019437.
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2000WO-US000376.
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99WO-US000106.
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 02-JUN-1998;
03-JUN-1998;
04-JUN-1998;
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18-JUN-1998;
18-JUN-1998;
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US2003022187-A1.
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04-70N-1998;
04-70N-1998;
04-70N-1998;
04-70N-1998;
06-70N-1998;
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06-70N-1998;
06-70N-1998;
06-70N-1998;
10-70N-1998;
10-70N-1998;
10-70N-1998;
11-70N-1998;
11-70N-1998;
11-70N-1998;
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20-MAR-1998
28-APR-1998
07-MAY-1998
02-UN-1998
02-UN-1998
                                                                                                                               14-NOV-2001;
                                                    Homo sapiens
                                                                                                                                                                   17-0CT-1997;
05-NOV-1997;
12-NOV-1997;
13-NOV-1997;
24-NOV-1997;
                                                                                                     30-JAN-2003
The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bloactive molecule to a cell expressing a PRO polypeptide, for linking a bloactive beloiogical activity of a cell. The PRO polypeptides or modulating at least on plantals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or abbits as targets for therapeutic intervention in certain cancers or rabbits as targets for therapeutic intervention in certain cancers (e.g. colon, lung or breast cancers) and diagnostic determination of the molecular weight markers or for formosome identification. The PRO genes are useful as hybridisation probes or for screening libraries of human control or mannaged the markers or for formosome identification. The PRO genes are useful as hybridisation probes or for screening libraries of human control or mannaged the properties and the sequences therapy, particularly for replacing a defective gene. The sequences therapy, particularly for replacing a defective gene. The sequences
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                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                            New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184, PRO361 or PRO846) useful as targets for therapeutic intervention in cancers (e.g. lung or breast cancers), or for diagnosing these cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLAALLGECVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
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Godowski P.
Paoni NF;
Wood WI;
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0
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                                                                                                                                                                       Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, "Watanabe CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
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                                                                                                                                                                                                                                                                                                                                    Claim 12; Fig 290; 647pp; English.
    23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000WO-US032678.
01-DEC-2000; 2000WO-US032678.
01-JUN-2001; 2001WO-US006520.
01-JUN-2001; 2001WO-US019692.
20-JUN-2001; 2001WO-US019665.
09-JUL-2001; 2001WO-US01966.
28-AUG-2001; 2001WO-US01966.
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Best Local Similarity 100.
Matches 104; Conservative
                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                       WPI; 2003-155950/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 104 AA;
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Zhang Z;
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### vaiolable antibody, cell death; tissue typing; gene therapy;

### Micckout animal; ammunohistochemical staining.

### Miccokout animal; ammunohistochemical staining.

### Micckout animal; ammunohistochemical staining.

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PR 24-TW-1998 9818-0090445 P
R 25-TW-1998 9818-009064 P
R 25-TW-1998 9818-009065 P
PR 01-TW-1998 9818-009114 P
PR 01-TW-1998 9818-009114 P
PR 02-TW-1998 9818-009514 P
PR
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MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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2000WO-US014941.
2000WO-US015264.
2000WS-0213637F.
2000WO-US02031.
            98WO-US019437.
98WO-US021141.
98WO-US021141.
99WO-US000106.
99WO-US000106.
99WO-US005028.
99WC-US005028.
99WC-US005028.
99WC-US005028.
99WC-US005028.
99WC-US013957P.
99WC-US013957P.
99WC-US01090.
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15-SEP-1999;
08-OCT-1999;
30-NOV-1999;
01-DEC-1999;
01-DEC-1999;
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98US-0090435P
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04-AUG-1998;
04-AUG-1998;
04-AUG-1998;
04-AUG-1998;
24 - 70x - 1998;
25 - 70x - 1998;
26 - 70x - 1998;
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26 - 70x - 1998;
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19-AUG-1998;
20-AUG-1998;
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31-AUG-1998;
16-SEP-1998;
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 retinal disorder, retinitis pigmentosum, kidney disorder, mammalian kidney mesangial cell proliferation; Berger disease, dermatitis, herperiformis; Crohn's disease, chondrocyte proliferation, chondrocyte redifferentiation, sports injury; arthritis.
                                                                           97405-0049787P

97405-00652186P

97405-00651186P

97405-0065111P

98405-00871008

98405-00871008

98405-00871008

98405-00871008

98405-00871008

98405-0088021P

98405-0088021P

98405-0088021P

98405-0088028P

98405-0089028P

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98405-0089028P

98405-0089599B

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98405-008959B

98405-008959B
                                                                 2001US-00990562
                                          US2003027985-A1
                                                                                 17-0CT-1997
12-NOV-1997
13-NOV-1997
13-NOV-1997
25-FEB-1998
26-FEB-1998
10-MAY-1998
10-JUN-1998
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24-JUN-1998;
24-JUN-1998;
                               Homo sapiens.
                                                                 14-NOV-2001;
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97105 - 0049787P - 97705 - 00492787P - 97705 - 0049278P - 9805 - 004927P - 9805 - 008927P - 9805 - 009927P - 9805
                           20-NOV-2001; 2001US-00989724
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28-MAY-1998;
02-JUN-1998;
02-JUN-1998;
02-JUN-1998;
03-JUN-1998;
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17-JUN-1998;
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23-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 104;
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100.0%; Pred. No. 1.4e-48;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                 16 DBC-1999; 99WC-US030095.
20-DBC-1999; 99WC-US0300911.
20-JAN-2000; 2000WC-US0300911.
06-JAN-2000; 2000WC-US030376.
11-FEB-2000; 2000WC-US003765.
11-FEB-2000; 2000WC-US004341.
22-FEB-2000; 2000WC-US004341.
24-FEB-2000; 2000WC-US005841.
10-MAR-2000; 2000WC-US005841.
10-MAR-2000; 2000WC-US005841.
11-MAR-2000; 2000WC-US005841.
20-MAR-2000; 2000WC-US005841.
21-MAR-2000; 2000WC-US01377.
30-MAR-2000; 2000WC-US01358.
11-MAR-2000; 2000WC-US01358.
11-MAR-2000; 2000WC-US01358.
                                          98WO-US021141

98WO-US025108

98WO-US025108

99WC-US005028

99WS-0141037P

99US-0141037P

99US-0141037P

99US-014304P

99US-014569B

99WS-014669B

99WS-014622P

99WS-0146236P

99WS-014623P

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99WS-014623P
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Best Local Similarity 100.
Matches 104; Conservative
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26. JUL-1999)
28. JUL-1999)
17. AUG-1999)
15. SEP-1999)
16. SEP-1999)
08. OCT-1999)
01. DEC-1999)
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    16-SEP-1998,
17-SEP-1998,
17-SEP-1998,
07-OCT-1998,
01-DEC-1998,
05-JAN-1999,
08-MAR-1999,
12-MAR-1999,
02-JUN-1999,
03-JUN-1999,
03-JUN-1999,
07-JUN-1999,
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98US-0090690P
98US-0090690P
98US-0090690P
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98US-0090693P
98US-0090863P
98US-0091863P
98US-009683P
98US-009689P
98US-00979P
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98US-00979P
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99WO-US005028,
99US-0123957P.
             25 - 70N - 1998
25 - 70N - 1998
26 - 70N - 1998
26 - 70N - 1998
26 - 70N - 1998
01 - 70L - 1998
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18-AUG-1998
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19-AUG-1998
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20-AUG-1998
26-AUG-1998
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12-MAR-1999;
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Human, PRO; secreted polypeptide, transmembrane polypeptide, toxin,
radiolabel; cell death, gene mapping, chromosome mapping,
protein electrophoresis, genetic disorder; immunosuppressive, cytostatic,
antibacterial.
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02-JUN-1999; 99WO-US012252.
23-JUN-1999; 99US-0141037P.
20-JUL-1999; 99US-0141037P.
20-JUL-1999; 99US-014568P.
28-JUL-1999; 99US-014568P.
28-JUL-1999; 99US-014568P.
17-AUG-1999; 99US-014568P.
15-SEP-1999; 99US-014563P.
16-DEC-1999; 99WO-US021547.
01-DEC-1999; 99WO-US021801.
01-MAR-2000; 2000WO-US0218378.
01-MAR-2000; 2000WO-US0218378.
01-MAR-2000; 2000WO-US0218328.
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16-JUN-1997; 97US-0049787P.
17-0CT-1997; 97US-0065216P.
12-NOV-1997; 97US-0065216P.
24-NOV-1997; 97US-0065211P.
24-NOV-1997; 97US-0065311P.
25-FEB-1998; 97US-0065311P.
26-MAY-1998; 98US-0075945P.
27-MAY-1998; 98US-0075945P.
28-MAY-1998; 98US-0075945P.
28-MAY-1998; 98US-0078910P.
28-MAY-1998; 98US-0088025P.
40-JUN-1998; 98US-0088026P.
40
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24-FEB-2000;
02-MAR-2000;
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The invention relates to a secreted and transmembrane polypeptide, termed responsible and the polynucleotide encoding it. The polypeptide is useful for detecting PRO polypeptides and for linking a bloactive molecule to a cell expressing the above polypeptides, where the bloactive molecule is a toxin radiolabel or an antibody. The bloactive material causes the death of the cell. The polypeptide, for preparative material causes the death of the cell. The polypeptide, for preparative material causes the death of the cell. The polypeptide, for propersis purposes of PRO, as a molecular weight marker for protein electrophoresis purposes and proparation of proparation of proparation probe, in chromosome and gene mapping, in generation of antisense RNA and DNA, in chromosome and gene mapping, in generation of antisense RNA and DNA, in chrowout animals which in turn are useful in the development and screening of therapeutically useful reagents, to construct hybridisation can analysis of individuals with genetic disorders, in gene therapy, for chromosome identification, as a chromosome marker and for generating namalysis. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.
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Godowski P.
Paoni NF;
Wood WI;
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Best Local Similarity 100.0%; Score 502; DB 6; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
Zhang Z;
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10-MAR-2000; 2000WO-US006319.
15-MAR-2000; 2000WO-US006884.
20-MAR-2000; 2000WO-US006884.
30-MAR-2000; 2000WO-US00884.37.
31-MAY-2000; 2000WO-US01358.
17-MAY-2000; 2000WO-US01358.
17-MAY-2000; 2000WO-US014941.
22-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US0252031.
24-AUG-2000; 2000WO-US03528.
08-NOV-2000; 2000WO-US03528.
01-DEC-2000; 2000WO-US03528.
01-DEC-2000; 2000WO-US035650.
20-JUN-2001; 2001WO-US035650.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US019692.
29-JUL-2001; 2001WO-US01136.
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N-PSDB; ABX17173.
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17-JUN-1998; 98US-0089653P.

18-JUN-1998; 98US-0089601P.

18-JUN-1998; 98US-0089601P.

18-JUN-1998; 98US-0089908P.

16-SEP-1998; 98US-0089908P.

17-SEP-1998; 98US-0089908P.

17-SEP-1998; 98US-0089908P.

16-SEP-1998; 98US-US013437.

05-JUN-1999; 98US-US01106.

08-MAR-1999; 99WS-US012108.

15-SEP-1999; 99WS-US012109.

16-DEC-1999; 99WS-US012109.

16-DEC-1998; 99WS-US012109.

16-DEC-1998; 99WS-US012109.

16-DEC-1998; 99WS-US012109.

16-DEC-1998; 99WS-US012109.

16-DEC-1998; 99WS
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Zhang Z;
     Human; secreted and transmembrane protein; gene therapy; PRO; PRO943; PRO183; PRO184; PRO185; PRO1813; PRO531; PRO531; PRO181; PRO1131; PRO511; PRO946; PRO1141; PRO7170; PRO361; PRO846; bioactive molecule; toxin; radiolabel; antibody; cell death; cancer; autoimmune disease; chromosome mapping; gene mapping; transgenic animal;
                                                                                                                                                                                                Novel human secreted and transmembrane protein PRO1245
                                                                                       ABU81693 standard; protein; 104 AA.
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9805-0088117P-
9805-00882117P-
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97US-0062250P.
97US-006511BP.
97US-0065111P.
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97US-0065111P.
98US-008460P.
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98US-008802FP.
98US-008802FP.
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98US-008802FP.
98US-008802FP.
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                                                                                                                                                               (first entry)
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17-OCT-1997)
15-NOV-1997)
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24-NOV-1997)
25-FEB-1998
26-ARX-1998
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ABU81693
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Botstein D, Desnoyers L,
                98US-0088217P-
98US-0088655P-
98US-0088734P-
98US-0088738P-
98US-0088738P-
98US-0088878P-
98US-0088878P-
98US-0088878P-
98US-0088878P-
98US-0089512P-
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98US-0089512P-
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99WO-US012252
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useful as a therapeutic agent e.g. for treating cancer and autoimmune disease. PRO is useful in assays to identify other proteins or molecules involved in binding interactions. The polymucleotide [II] encoding (I) is useful in chromosome and gene mapping, for generating transgenic animals or knockout animals which in turn are useful in the development and individuals with genetic disorders, in gene therapy, for the genetic analysis of individuals with genetic disorders, in gene therapy, for chromosome identification, and as a chromosome marker. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g. detecting its expression in specific cells, tissues or serum, for affinity purification in for treating septic shock. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
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                                                                                                                                                                                               1 MKLAALLIGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Human; gene therapy; cancer; retinal disorder; wound healing; kidney disorder.
                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                        LSSLGIPVNHLIEGSOKCVAELGPQAVGAVKALKALLGALTVFG 104
                                                                                                                                                                                                                                                    LSSLGIPUNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
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97US-0062250P.
97US-00651186P.
97US-0065311P.
97US-0065311P.
98US-0078945P.
98US-0078945P.
98US-0081322P.
98US-0081322P.
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98US-0088030P.
98US-0088033P.
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                                                                                                                                                                                                                                                                                                                                                         11-AUG-2003 (first entry)
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                                                                                                                                         Sequence 104 AA;
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12-NOV-1997)
13-NOV-1997)
24-NOV-1997)
25-FEB-1998
26-MAX-1998
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28-MAX-1998
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04-JUN-1998
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Eaton DL;

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28-MAY-1998;
02-JUN-1998;
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The invention relates to an isolated nucleic acid encoding a PRO polypeptide, agonist, antagonist and antibody are useful for the preparation of a medicament for treating a condition that is responsive to the PRO polypeptide. The nucleotide sequence is useful in chromosome and gene mapping used as hybridisation probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. The PRO polypeptides can also be used in the treatment of e.g. cancer, retinal disorders, wound healing and kidney disorders. The present sequence represents the amino acid sequence of a human secreted sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at sequence.
                                                                                     New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for the preparation of a medicament for treating a condition that is responsive to the PRO polypeptide. e.g., cancer.
                                                                                                                                                                                                                                                                                                                                                                                              1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
                                                                                                                                                                                                                                                                                                                                                                            1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
  Godowski PJ;
           Paoni NF;
Wood WI;
                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, PRO polypeptide, secreted protein; transmembrane protein; blosensor; bioreactor; tumour, cancer; diabetes; ALS; ulcer; rheumatoid arthritis; amyotrophic lateral sclerosis; cytostatic; antidiabetic; antiathritic; antirheumatic; antiulcer.
                                                                                                                                                                                                                                                                                                                                    Length 104;
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, (Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
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100.0%; Pred. No. 1.4e-48;
vative 0; Mismatches 0;
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                                                                                                                                   Claim 12; Fig 290; 647pp; English.
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97US-0062250P.
97US-0065186P.
97US-006511P.
97US-0066770P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PRO1245 polypeptide.
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Matches 104; Conservative
                                                       WPI; 2003-370792/35.
N-PSDB; ACA88477.
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05-NOV-1997;
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                                   Zhang Z;
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ABO34146
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9805 0090540P 9805 0090542P 9805 0090676P 9805 0090676P 9805 0090694P 9805 0090694P 9805 0090695P 9805 0090695P 9805 0090695P

98US-0091544P. 98US-0091478P. 98US-0091519P.

98US-0078910P.
98US-0081322P.
98US-0087106P.
98US-0087106P.
98US-0087159P.
98US-0087759P.
98US-008022P.
98US-008022P.
98US-008022P.
98US-008023P.
98US-00803S.

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PR 02_UUL_1999; 98US-0031633P.
PR 07_UUL_1999; 98US-0031633P.
PR 09_UUL_1999; 98US-0032132P.
PR 20_UUL_1999; 98US-0032132P.
PR 20_UUL_1999; 98US-0032132P.
PR 04_AUG_1999; 98US-003532P.
PR 04_AUG_1999; 98US-003532P.
PR 04_AUG_1999; 98US-003531P.
PR 10_AUG_1999; 98US-003531P.
PR 10_AUG_1999; 98US-003531P.
PR 10_AUG_1999; 98US-003531P.
PR 10_AUG_1999; 98US-003531P.
PR 11_AUG_1999; 98US-003532P.
PR 26_AUG_1999; 98US-003532P.
PR 26_AUG_1999; 98US-003732P.
PR 26_AUG_1999; 98US-003733P.
PR 26_AUG_1999; 98US-003739P.
PR 26_AUG_1999; 98US-003739P.
PR 26_AUG_1999; 98US-003739P.
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MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTINPLKLL
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100.0%; Score 502; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0;
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97US-0062250P.
97US-US020069.
97US-0065186P.
97US-0065311P.
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2000WO-US02352
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2000WS-02309789
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2000WO-US030952
2001WO-US0305678
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2000WO-US014042
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05-JAN-2000; 2

18-FBB-2000; 2

18-FBB-2000; 2

22-FBB-2000; 2

24-FBB-2000; 2

24-FBB-2000; 2

24-FBB-2000; 2

24-FBB-2000; 2

15-MAR-2000; 2

15-MAR-2000; 2

15-MAY-2000; 2

15-MAY-2000; 2

22-MAY-2000; 2

23-MIN-2000; 2

24-MIN-2000; 2
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17-OCT-1997;
05-NOV-1997;
12-NOV-1997;
13-NOV-1997;
24-NOV-1997;
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98US-0075945P

98US-0083910P

98US-0087100P

98US-0087100P

98US-008710P

98US-0088011P

98US-0088025P

98US-0088020P

98US-0088025P

98US-0088025P

98US-0089020P

98US-0089020P
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99WO-US028834.
99WO-US028834.
99WO-US030095.
200WO-US000219.
200WO-US000376.
25-FBB-1998,
26-APR-1998,
26-APR-1998,
07-MAY-1998,
08-JUN-1998,
02-JUN-1998,
04-JUN-1998,
04-JUN-1998,
04-JUN-1998,
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04-JUN-1998,
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05-JUN-1998,
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10-JUN-1998;
10-JUN-1998;
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The invention relates to an isolated mucleic acid molecule comprising the full-length coding sequence of the DNA ATCC Accession Numbers given in the specification, or comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 147 PRO polypeptides, or an extracellular domain of the polypeptide; or (b) any of 147 nucleotide sequences fully defined in the specification. Also included are the PRO proteins (or their extracellular domains), expression vectors, host cells, PRO chimaeric proteins, anti-PRO antibodies, methods of detecting polypeptide in a sample, methods of mithodies, methods of detecting polypeptide in a sample, methods of inking a bioactive molecule to a cell expressing a polypeptide and methods of modulating at least one biological activity of a cell expressing the polypeptide. The PRO polypeptides or coll expressing a polymocleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are useful for stimulating hypertrophy of neonatal catch, promoting anglogenesis, inhibiting vascular endothelial grawinal or factor (VEGP)-stimulated proliferation of endothelial cells, modulating glucose or FPA uptake by adipocyte colliferation of stimulated T-lymphocytes, enhancing the survival or for inducing proliferation and/or re-differentiation. In particular, these are useful for detecting or treating tumours and certain cancers (colon, lung or breast cancers) in mammals, e.g. humans, colling a defective corration seates, sheep, pigs, goats, or rabbits. The PRO genes may also be used in gene therapy, particularly for replacing a defective corration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
                                                                                                                                                                                                                                                                                                                                                                                       DL;
Godowski PJ;
Paoni NF;
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated PRO183, PRO184, PRO361 or PRO846 nucleic acid and secreted transmembrane polypeptides, useful as targets for the diagnosis and treatment of cancers, such as lung and breast cancers.
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100.0%; Score 502; DB 6; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                         Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton
Berzara N, Fong S, Gerber H, Gerzitsen ME, Goddard A,
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Fig 290; 660pp; English.
30-MAY-2000, 2000WO-US014941.
02-UTW-2000, 2000WO-US015264.
28-UJU-2000, 2000WO-US020011.
11-AUG-2000, 2000WO-US022031.
23-AUG-2000, 2000WO-US023522.
24-AUG-2000, 2000WO-US023928.
08-NOY-2000, 2000WO-US03952.
01-DEC-2000, 2000WO-US039652.
01-DEC-2001, 2001WO-US019692.
20-UJW-2001, 2001WO-US019692.
20-UJW-2001, 2001WO-US019692.
29-UJW-2001, 2001WO-US01166.
09-UJU-2001, 2001WO-US021066.
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N-PSDB; ADA37918.
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Zhang Z;
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61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104

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AMOUNT 24

AMOUNT 24

AMOUNT 2015

AMOUNT 20
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PR 116-UNN-1998 BUS-0069940PP PR 19-UNN-1998 BUS-0069940PP PR 19-UNN-1998 BUS-0069940PP PR 19-UNN-1998 BUS-0069940PP PR 20-UNN-1998 BUS-0069940PP PR 20-UNN-1998 BUS-0069940PP PR 22-UNN-1998 BUS-0069940PP PR 22-UNN-1998 BUS-0069940PP PR 22-UNN-1998 BUS-006942PP PR 22-UNN-1998 BUS-006942PP PR 23-UNN-1998 BUS-006942PP PR 23-UNN-1998 BUS-006942PP PR 23-UNN-1998 BUS-006942PP PR 24-UNN-1998 BUS-006942PP PR 25-UNN-1998 BUS-006942PP PR 25-UNN-1998 BUS-006967PP PR 25-UNN-1998 BUS-006969PP PR 25-UNN-1998 BUS-00
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(first entry)

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ADA10392 standard; protein; 104 AA
                     06-NOV-2003
           ADA10392
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                                                                                                                                                                                                                                                                                                                                                   1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
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                                                                                                                                                                                                                                                                                                                                                                        LSSLGIPVNHLIEGSOKCVAELGPOAVGAVKALKALLGALTVFG 104
                                                                                                                                                                                                                                                                                                                                                                               LSSLGI PVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
98US - 0097661P.
98US - 0097952P.
98US - 0097952P.
98US - 0097952P.
98US - 0097974P.
98US - 0108858P.
98US - 0108858P.
98US - 0108858P.
99WO - USO1141.
99WO - USO21141.
99WO - USO21141.
99WO - USO21141.
99WO - USO2114.
99US - 0144758P.
99US - 0146336P.
99US - 0146336P.
99WO - USO211690.
99WO - USO211690.
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RESULT 25 ADA10392

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PRO; secreted protein; transmembrane protein; human; septic shock;
Human secreted/transmembrane protein, PRO1245.
                                                                                                                                                                           97US-0049787P.
97US-0062250P.
97US-0065211P.
97US-0065311P.
98US-0065311P.
98US-0075947P.
98US-0075947P.
98US-0084600P.
98US-0081702P.
98US-0081702P.
98US-008172P.
98US-008172P.
98US-0088028P.
98US-0089028P.
98US-0089028P.
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98US-0089952P.
98US-0090246P.
                                                                                                                                                     2001US-00989729
                                                                                             US2003059831-A1
                                                                   Homo sapiens.
                                                                                                                                                   19-NOV-2001;
                                                                                                                        27-MAR-2003
                                         immunogen.
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98US-0090254P. 98US-00901349P. 98US-00901349P. 98US-00901349P. 98US-00901349P. 98US-0090431P. 98US-0090431P. 98US-0090444SP. 98US-0090444SP. 98US-0090444SP. 98US-0090444SP. 98US-0090444SP. 98US-009054P. 98US-0090554P. 98US-0090554P. 98US-0090554P. 98US-0090554P. 98US-0090554P. 98US-009054P. 98US-009054P. 98US-009054P. 98US-009054P. 98US-009054P. 98US-009151P. 98US-009151P. 98US-0091628P. 98US-0091628P. 98US-0091628P. 98US-0091628P. 98US-0091628P. 98US-0091628P. 98US-0091633P. 98US-0091633P. 98US-0091633P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0091638P. 98US-0092182P. 98US-0092182P. 98US-0092182P. 98US-0092182P. 98US-0092182P. 98US-0092182P. 98US-0092182P. 98US-0092182P. 98US-0092182P. 98US-009531EP.	1018-0096146] 1018-0096126] 1018-0096126] 1018-0096126] 1018-0096126] 1018-0096126] 1018-0096126] 1018-0096126] 1018-0096126] 1018-0096126] 1018-0096126] 1018-0096126] 1018-0096126] 1018-0096126] 1018-0096126] 1018-0096126] 1018-0096126] 1018-0097126] 1018-0097126] 1018-0097126] 1018-0097126] 1018-0097126] 1018-0097126] 1018-0097126] 1018-0097126] 1018-0097126] 1018-0097126] 1018-0097126] 1018-0097126] 1018-0097126] 1018-0097126] 1018-0097126] 1018-0097126] 1018-0097126] 1018-0097126]
PR 22-JUN-1998 PR 23-JUN-1998 PR 24-JUN-1998 PR 25-JUN-1998 PR 26-JUL-1998 PR 26-	R 11.AUG-1999 R 17-AUG-1999 R 11-AUG-1999 R 11-AUG-1999 R 18-AUG-1999 R 18-AUG-1999 R 18-AUG-1999 R 18-AUG-1999 R 26-AUG-1999 R 26-AUG-1999 R 26-AUG-1999 R 26-AUG-1999

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1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
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Best Local Similarity 100.0%; Pred. No. 1.4e-48; Length 104;
Matches 104; Conservative 0; Mismatches 0; Indels (
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98US-0097978P.
98US-0097979P.
98US-0097979P.
98US-0097825P.
98US-0098014P.
98US-0098625P.
98US-01068825P.
98US-0106888P.
98US-0106888P.
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99US-0141037P.
99US-014037P.
99US-01608037F.
99US-01608037F.
99US-01608037F.
90US-01608037F.
                                                                                                                                      17-SEP-1998; 07-OCT-1998; 07-OCT-1998; 08-MAN-1999; 08-MAN-1999; 08-MAN-1999; 08-MAN-1999; 08-MAN-1999; 08-MAN-1999; 08-UUL-1999; 08-UUL-1999; 08-UUL-1999; 08-UUL-1999; 08-UUL-1999; 08-UUL-1999; 08-UUL-1999; 08-UUL-1999; 08-MAN-2000; 22-FEB-2000; 22-FEB-2000; 22-FEB-2000; 22-FEB-2000; 23-MAN-2000; 23-MA
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ADA17936 standard; protein; 104 AA.

RESULT 26 ADA17936 ID ADA17 XX AC ADA17

ADA17936

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9805-0090431P-
9805-0090431P-
9805-00904431P-
9805-00904445P-
9805-00904445P-
9805-00904445P-
9805-00904445P-
9805-00904445P-
9805-0090642P-
9805-009144P-
9805-0090642P-
9805-0091444P-
9805-0090642P-
9805-0090642P-
9805-0090642P-
9805-0090644P-
9805-0090644P-
9805-0090644P-
9805-009644P-
9805-00964P-
98US-0090355P
                                                                                                   Human; PRO polypeptide; secreted protein; transmembrane protein;
transgenic; tumour; cytostatic.
                                                                                                                                                                                                                                                                                                                                 9705-0042787P

9705-0062216P

9705-0065111P

9705-0065111P

9705-0065111P

9705-0065111P

9805-0078942P

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9805-008721P

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9805-0088021P

9805-0088028P

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9805-0089028P
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                            20-NOV-2003 (first entry)
                                                                      Human PRO1245 polypeptide
                                                                                                                                                                                                               US2003054987-A1.
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28-MAY.1998;

28-MAY.1998;

22-UN.1998;

22-UN.1998;

23-UN.1998;

24-UN.1998;

24-UN.1998;

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24-UN.1998;

24-UN.1998;

24-UN.1998;

24-UN.1998;

25-UN.1998;

26-UN.1998;

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PRO; secreted protein; transmembrane protein; hypertrophy of neonatal heart; angiogenesis; vascular endothelial growth factor; VEGF-stimulated proliferation; vascular endothelial growth factor; VEGF-stimulated proliferation; red photoreceptor cell; c-fos induction; adipocyte cell; phondrocyte differentiation; pancreatic beta-cell precursor differentiation; cardiac insufficiency disorder; wound; cancerous tumour; cardiac insufficiency disorder; wound; cancerous tumour; cardiac insufficiency disorder; hyperinsulinaemia, hypoinsulinaemia; bone disorder; cartilage disorder; sports injury; arthritis; cancer; human.
Human secreted/transmembrane protein PRO1245.
                                                                                                                                                                                                                                                                                                                                         97105-0049787P.
97105-00622160P.
97105-0065111P.
97105-0065111P.
97105-0065111P.
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97105-0065111P.
97105-0065111P.
97105-0065111P.
97105-0065111P.
97105-0065112P.
97105-0081021P.
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02-JUN-1998;
03-JUN-1998;
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10-JUN-1998;
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11-JUN-1998;
11-JUN-1998;
11-JUN-1998;
                                                                                                                                                                                                                       Homo sapiens
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28-MAY-1998;
02-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
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10-MAR-2000; 2000WO-US006819.

15-MAR-2000; 2000WO-US006819.

30-MAR-2000; 2000WO-US008139.

15-MAY-2000; 2000WO-US013368.

17-MAY-2000; 2000WO-US013705.

22-MAY-2000; 2000WO-US014042.

30-MAY-2000; 2000WO-US014042.

30-MAY-2000; 2000WO-US014941.

22-UN-2000; 2000WO-US015264.

23-UN-2000; 2000WO-US015264.

24-UN-2000; 2000WO-US015264.

25-UN-2000; 2000WO-US015264.
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99WO-US02834
99WO-US028634
99WO-US030915
200WO-US000316
2000WO-US00376
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2000WO-US004414.
2000WO-US004914.
2000WO-US005004.
2000WO-US005841.
     98US-0098014P.
98US-0109852FP.
98US-010085RP.
98WO-US019330.
98WO-US019437.
98WO-US019437.
98WO-US02108.
99WO-US025108.
99WO-US02528.
99WO-US025252.
99US-014304P.
99US-014569P.
99US-014569P.
99WS-014569P.
99WS-014569P.
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      26-AUG-1998;

16-SEP-1998;

16-SEP-1998;

17-SEP-1998;

17-SEP-1998;

17-SEP-1998;

17-SEP-1998;

16-SEP-1998;

16-SEP-1999;

16-AUL-1999;

16
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Best Local Simi
Matches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA28044;
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ADA28044
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PR 22-JUN-1998 99US 000024PP PR 22-JUN-1998 99US 000024PP PR 22-JUN-1998 99US 000024PP PR 23-JUN-1998 99US 000024PP PR 23-JUN-1998 99US 000024PP PR 24-JUN-1998 99US 000035PP PR 24-JUN-1998 99US 000035PP PR 24-JUN-1998 99US 000043PP PR 25-JUN-1998 99US 000043PP PR 25-JUN-1998 99US 000043PP PR 25-JUN-1998 99US 000065PP PR 25-JUN-1998 99US 000069PP PR 25-JUN-1998 99US 000069PP PR 25-JUN-1998 9
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MKI.AAILIGI.CVALISCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 502; DB 6; Best Local Similarity 100.0%; Pred. No. 1.4e-48; Matches 104; Conservative 0; Mismatches 0;
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26-AUG-1998, 98US-0097955P.
26-AUG-1998, 98US-0097971P.
26-AUG-1998, 98US-0097974P.
26-AUG-1998, 98US-0097978P.
26-AUG-1998, 98US-0097978P.
26-AUG-1998, 98US-0097978P.
26-AUG-1998, 98US-0097978P.
26-AUG-1998, 98US-0100858P.
17-SEP-1998, 98US-0100858P.
17-SEP-1998, 98US-0100858P.
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17-SEP-1998, 98US-0100858P.
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18-MAR-1999, 99US-0141037P.
19-UUL-1999, 99US-01456834.
19-UUL-1999, 99US-01456834.
19-UUL-1999, 99US-0156634.
19-UUL-1999, 99US-0156634.
11-FEB-2000, 2000WO-US001319.
11-FEB-2000, 2000WO-US001319.
11-FEB-2000, 2000WO-US001319.
11-MAR-2000, 2000WO-US001319.
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18-09-99/-428-408.rad

hypertrophy of neonatal heart, angiogenesis, lated proliferation; vascular endothelial growth factor; VEGF-stimulated proliferation; endothelial cell; T-lymphocyte proliferation; retinal neuron; c-fos induction; adipocyte cell; chondrocyte differentiation; pancreatic beta-cell precursor differentiation; gene therapy; tumour; cancer; human; colon cancer; lung cancer; breast cancer; cod photoreceptor cell.

Homo sapiens.

US2003059832-A1

27-MAR-2003

15-NOV-2001; 2001US-00

7US-0049787	7US-0062250	7WO-US02006	7US-0065186	7US-0065311	0113-0066770	BUS-0075945	8US-0078910	SUS-0083322	8US-0084600	8US-0087106	8US-0087607	808-808 808-808	808-000/030	JS-0087827	8US-0088021 8TS-0088025	8118-0088026	8118-0088028	8US-0088029	8US-0088030	BUS-0088033	8US-008B326	8US-0088167	8US-0088202	8US-0088212	8US-0088217	8US-0088655	803-0068/3# 8113-0088738	BUS-0088742	8US-0088810	BUS-0088824	BUS-0088826	8US-0088858	BUS-0088861	8US-0088876	8US-0089105	808-0089440	8US-0089312	8US-0089532	8US-0089538	80S-0089598	8US-0089599	US-0089600	8US-0089653		808-008990/ 8118-0089908	BUS-0089947	8US-0089948	8US-0089952	8US-0090246	8US-0090252	98US-0090254P.	8US-0090349	
- 3UN-199	7-OCT-199	S-NOV-199	2-NOV-199	3-NOV-199	4-NOV-199	5-FEB-199	0-MAR-199	3-APR-199	7-MAY-199	3-MAY-199	2-JUN-199	2-JUN-199	2 - NOO - 2	0 - NUD - 19	90 (- NITE: - 4	2	201 - NIT 4	4-VUV-199	4-JUN-199	4-JUN-199	4-JUL-199	5-JUN-199	5-UUT-199	5-UUV-199	5-NUT-3	9-1-NDD-6	201-NTT:-0	0-11N-199	961-NDD-0	0-JUN-199	0-JUN-199	1-JUN-199	1-NUV-199	1-JUN-199	2-ND-199	PAT-NOO-9	0 0 1 - MTT A	96T-NDD-7	7-JUN-199	99,1-NUT-7	7-JUN-199	1991-NUD-7	961-NUD-7	SOL MUDI-B	B-CON-LWS	9-1100-0	661-NDD-6	9-JUN-199	2-JUN-199	2-JUN-199	22-JUN-1998;	3-JUN-199	
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9805-009059P.

23 - TUN - 1998 | 24 - TUN - 1998 | 25 - TUN - 1998 | 26 - TUN - 1

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9705-0049787P

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98US-0089948P.
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98US-0090472P.
98US-0090535P.
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                                                             14-NOV-2001; 2001US-00991854
            US2003059780-A1.
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28-MAY-1998;
02-JUN-1998;
                                    27-MAR-2003
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100.0%; Score 502; DB 6; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels
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06-JAN-2000; 2000WO-US000376.
118-FEB-2000; 2000WO-US000376.
22-FEB-2000; 2000WO-US004144.
24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US004914.
26-MAR-2000; 2000WO-US006819.
15-MAR-2000; 2000WO-US006819.
15-MAR-2000; 2000WO-US006819.
15-MAR-2000; 2000WO-US008139.
17-MAR-2000; 2000WO-US013358.
17-MAR-2000; 2000WO-US013358.
98US-0098014P.
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98US-0100858P.
98WO-US019330.
98WO-US019437.
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ADA38849
    SXXXXXXXXXXXX
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MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEBAGGTLANPLGTLNPLKLL
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Pred. No. 1.4e-48;
0; Mismatches 0;
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99WO-USO00106.
99WO-USO05028.
99WS-0123957P.
99WS-0141037P.
99US-0141037P.
99US-0144758P.
99US-0144758P.
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99US-0144758P.
99US-0146598P.
99WS-0146598P.
99WS-0146598P.
99WO-USO11547.
99WO-USO11547.
99WO-USO28813.
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Best Local Similarity 100.0%;
Matches 104; Conservative 0;
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2000WO-US00365.
2000WO-US004414.
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2000WO-US022031.
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2000US-0230978P.
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      05-JAN-1999;

08-MAR-1999;

08-MAR-1999;

23-JUN-1999;

20-JUL-1999;

26-JUL-1999;

15-SEP-1999;

11-AUG-1999;

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      rod photoreceptor cell
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                              Homo sapiens,
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                               12-DEC-1999

99W-0-US010106

05-JAN-1999

99W-0-US010228-1

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99W-0-US01225-2

20-JUL-1999

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15-SEP-1999

99W-01236F9-1

15-SEP-1999

99W-01236F9-1

16-DEC-1999

99W-0-US0199-1

99W-0-US019-1

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98MO-US022108
98MO-U11325108
98MO-US0201066.
99MO-US05028.
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1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGGTLANPLGTLNPLKLL
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100.0%; Pred. No. 1.4e-48;
iive 0; Mismatches 0;
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08-MAR-1999; 99WO-USO0528.

02-JUN-1999; 99WS-0123957P.

02-JUN-1999; 99WS-0141037P.

20-JUL-1999; 99WS-0141037P.

20-JUL-1999; 99WS-0145688P.

26-JUL-1999; 99WS-0145688P.

15-SEP-1999; 99WS-0146522P.

15-SEP-1999; 99WS-013965113.

01-DEC-1999; 99WC-USO21990.

01-DEC-1999; 99WC-USO218913.

01-DEC-1999; 99WC-USO219911.

02-JAN-2000; 200WWC-USO021965.

11-FEB-2000; 200WWC-USO03165.

12-FEB-2000; 200WWC-USO0366114.

24-FEB-2000; 200WWC-USO0366119.

15-MAR-2000; 200WWC-USO06884.

10-MAR-2000; 200WWC-USO06884.

11-MAR-2000; 200WWC-USO06889.

15-MAR-2000; 200WWC-USO0689.

15-MAY-2000; 200WWC-USO013358.

15-MAY-2000; 200WWC-USO13358.

15-MAY-2000; 200WWC-USO13358.

12-MAY-2000; 200WWC-USO13358.

23-JUW-2000; 200WWC-USO13358.

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97US-0065311P.
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98US-0078910P.
98US-0084600P.
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98US-0088028P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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; Pred. No. 1.4e-48;
0; Mismatches 0;
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                                   15-58P-1999; 990G-0149366P.
15-58P-1999; 990G-015021090.
15-58P-1999; 990G-015021090.
15-58P-1999; 990G-0158653P.
30-NOV-1999; 990G-0158653P.
30-NOV-1999; 990G-0158653P.
30-NOV-1999; 990G-0158028313.
30-NOV-1999; 990G-015028834.
30-NOV-1999; 990G-015028834.
30-NOV-1999; 990G-015028834.
30-NOV-1999; 990G-015028834.
30-NOV-1999; 990G-01502893.
30-NOV-1999; 990G-01502893.
30-NOV-1999; 990G-01502893.
30-NOV-1999; 990G-01502893.
30-NOV-1999; 990G-01502893.
30-NOV-1999; 990G-0150293.
30-NOV-1999; 990G-0150293.
30-NOV-1999; 990G-0150293.
30-NOV-1999; 990G-0150293.
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15-MAR-2000; 2000MO-US005619.
20-MAR-2000; 2000MO-US005684.
30-MAR-2000; 2000MO-US00439.
15-MAY-2000; 2000MO-US01358.
17-MAY-2000; 2000MO-US01358.
22-MAY-2000; 2000MO-US014941.
30-MAY-2000; 2000MO-US014941.
31-MAY-2000; 2000MO-US014941.
32-JUN-2000; 2000MO-US012564.
33-JUN-2000; 2000MO-US012564.
33-JUN-2000; 2000MO-US012564.
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99US-0144758P.
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99WO-US028313.
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2000WO-US005004.
2000WO-US005811.
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2000WO-US006884.
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Best Local Similarity
Matches 104; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003017982-A1
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17-OCT-1997;
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human; tissue typing; cardiac insufficiency disorder; angiogenesis; wound healing; tumour; immune response; retinal disorder; retinal injury; sight loss; age-related macular degeneration; Amb. kidney disorder; mesangial cell function; Berger disease; nephropathy; dermatitis; herpetiform; Crohn's disease; sports injury; arthritis.
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PR 03-JUL-1998; 980S-0091273P.

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PR 11-AUG-1998; 980S-009561P.

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PR 26-JUL-1999; 98US-01078B.P.
PR 26

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98US-008727P.
98US-0088021P.
98US-0088028P.
98US-008902P.
98US-008903P.
98US-0090349P.
98US-0090349P.
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9803-0090690P.
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98US-0091978P.
96US-0091982P.
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100.0%; Pred. No. 1.4e-48;
ive 0; Mismatches 0;
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   05-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000376.
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12-FEB-2000; 2000WO-US004341.
22-FEB-2000; 2000WO-US004914.
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25-MAY-2000; 2000WO-US0136770.
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25-MAY-2000; 2000WO-US0136377.
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98US-008312P.
98US-0087106P.
98US-0087106P.
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Matches 104; Conservative
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17-CCT-1997;
12-NOV-1997;
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13-NOV-1997;
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20-ARX-1998;
07-MAY-1998;
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PR 09-7UL 1998; 98US-0092132P.
PR 10-1UL 1999; 98US-0092472P.
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PR 30-UUL 1998; 98US-0092472P.
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Pred. No. 1.4e-48;
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Best Local Similarity 100.0%; Pred. No. 1.4
Matches 104; Conservative 0; Mismatches
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98US-0087106P.
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17-OCT-1997;
12-NOV-1997;
13-NOV-1997;
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25-NOV-1997;
26-MAR-1998;
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07-MAY-1998;
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02-JUN-1998;
03-JUN-1998;
04-JUN-1998;
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ADC55252
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8US - 0088028 8US - 0088028 8US - 0088030 8US - 0088030 8US - 0088167 8US - 0088167 8US - 0088217 8US - 0088217 8US - 0088742 8US - 0088742	8 US - 0 0 8 8 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	98US-0090349P. 98US-0090435P. 98US-00904431P. 98US-00904435P. 98US-0090445P. 98US-0090445P. 98US-0090540P. 98US-0091544P. 98US-0091544P. 98US-0091548P.
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98US-0094651P.
98US-0095282P.
98US-0095282P.
98US-0095302P.
98US-0095301P.
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20 - JUL - 1998 | 04 - AUG - 1998 | 05 - AUG - 1998 | 07 - AUG - 1999 | 07 - AUG - 1

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98US-0088028P

98US-0088028P

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llarity 100.0%; Pred. No. 1.4e-48;
Conservative 0; Mismatches 0;
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98US-0083122P.
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98US-008312P.
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2000WO-US022031.
2000WO-US023522.
           2000WO-US005841.
2000WO-US006319.
2000WO-US006884.
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2000WO-US008439.
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2000WO-US014941
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  2000WO-US005004
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Matches 104; Conserv
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23-UNN-2000;
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28-APK-1998;
02-MAY-1998;
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04-JUN-1998;
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PR 74-AUG-1999; 99US-005522P.
PR 74-AUG-1999; 99US-005522P.
PR 74-AUG-1999; 99US-005521P.
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PR 74-AUG-1999; 99US-005531P.
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PR 26-
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Matches 104; Conservative 0; Mismatches 0;
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24-FEB-2000; 2000WO-US005004.
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04-JUN-1998;
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04-JUN-1998;
04-JUN-1998;
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RR 05-UNN-1998; 98US-0088167P.
RR 05-UNN-1998; 98US-0088202P.
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PR 11-AUG-1998 | 98US-0056758P
PR 11-AUG-1998 | 98US-0056959P
PR 12-AUG-1998 | 98US-0056959P
PR 26-AUG-1998 | 98US-0056959P
PR 26-AUG-1998 | 98US-0056959P
PR 26-AUG-1998 | 98US-0056959P
PR 26-AUG-1998 | 98US-0059791P
PR 26-AUG-1998 | 98US-0097941P
PR 26-AUG-1998 | 98US-0103256P
PR 26-AUG-1999 | 99US-014358P
PR 26-AUG-19

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PR 15-MAY-2000; 2000WG-US01358.

PR 22-MAY-2000; 2000WG-US013705.

PR 20-MAY-2000; 2000WG-US01404.2

PR 30-MAY-2000; 2000WG-US014941.

PR 23-UJN-2000; 2000WG-US014641.

PR 23-UJN-2000; 2000WG-US012664.

PR 23-UJN-2000; 2000WG-US020710.

PR 11-AUG-2000; 2000WG-US02031.

PR 23-AUG-2000; 2000WG-US023522.
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: April 5, 2004, 14:34:07 Job time : 58 secs

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O53209 mycobacteri Q8x800 raletonia s Q8dqm0 synechococc P18825 homo sapien P24230 escherichia Q12955 homo sapien P30233 bradyrhizob Q58091 methanococc P07916 gallus gall	P55128 actinobacil P55129 actinobacil O33431 porphyromon P15320 serratia ma Q9490 homo sapien Q8pws2 methanosarc Q9uurs aspergillus Q82098 anabaena sp Q8uuhl agrobacteri P77596 escherichia P010102 pseudomonas Q9h2x8 homo sapien P30763 mycobacteri	QQBDB9 xanthomonas Q9y8t2 aeropyrum p Q8x4v6 escherichia P59918 prochloroco Q9ccs6 mycobacteri P71789 mycobacteri P7178 mycobacteri P55772 rhizoblum s Q51772 pseudomonas P08318 human cytom P31500 mycobacteri O53268 mycobacteri O13287 candida alb P54277 homo sapien Q9rxy1 deinococus	Q10396 mycobacteri Q9a4G3 caulobacter Q64355 mus musculu Q8nt28 oryyabacte Q9mf5 oryyabacte Q9mf1 halobacteri P54795 klebsiella Q9446 dictyosteli P71884 mycobacteri D71884 mycobacteri D71884 coturnix co Q92154 pharbitis n P3247 pharbitis n P3247 pharbitis n P3247 pharbitis n P3247 pharbitis n P3247 partomyce Q92184 coturnix co Q8nff8 coturnix co Q8nff8 coturnix co Q8nff8 drosophila P11536 drosophila P11536 drosophila Q8uf68 agrobacteri P4106 bucella me Q8uf65 haemophilus P23554 xanthomonas Q9uf70 homo sapien P26924 azospirillu P78426 homo sapien
ненанана	ченеенененене	енанананананана	361 1 COBT_MYCTU 511 1 NABB_CAUCR 560 1 EPS MOUSE 760 1 CO2_MOUSE 129 1 ILLI_RAT 242 1 HIS4_HALN1 257 1 MORE KLEAE 299 1 TLI_RAD 382 1 YN28_MYCTU 382 1 YN28_MYCTU 383 1 CHSD_PHANI 668 1 YNZ8_MYCTU 660 1 SMP_COTUA 660 1 TXT_XANFL 75 1 YTXI_XENLA 668 1 TXT_XANFL 75 1 YTXI_XENLA 76 1 DDL_FAEIN 76 1 TXT_XANFL 76 1 TXT_XANFL 77 1 YTXI_XENLA 76 1 TXT_XANFL 76 1
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compuge OM protein - protein search, using sw model Run on: April 5, 2004, 14:11:13 ; Search ti	Title: Perfect score: 502 Sequence: 1 MKLAALLGLCVALSCSSAAAQ Scoring table: BLOSUM62 Searched: 141681 seqs, 52070155 residues Total number of hits satisfying chosen parameters Minimum DB seq length: 0 Maximum DB seq length: 200000000	ocessing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries e: SwissProt_42:* red. No. is the number of results predicore greater than or equal to the score and is derived by analysis of the total Score Match Length DB ID Score Match Length DB ID	1 497 99.0 104 1 UGRZ_HUMAN 4 135 26.9 139 1 UGRZ_HUMAN 4 135 26.9 139 1 UGRZ_HUMAN 5 26.9 139 1 UGRZ_HUMAN 6 135 26.9 139 1 UGRZ_HUMAN 6 135 16.5 1327 1 TNKI_HUMAN 7 15.3 335 1 TRDZ_GTRCO 7 7 6 15.1 3 32 1 COPA_HELE 7 14.9 362 1 MDCI_MUUSE 10 7 4 14.7 779 1 SNLL_MOUSE 11 73.5 14.6 626 1 DXS_MIGBR 7 14.9 362 1 MDCI_MUUSE 11 73.5 14.6 626 1 DXS_MIGBR 7 14.1 428 1 SNLC_MOUSE 11 73.5 14.6 626 1 DXS_MIGBR 7 1 14.1 428 1 SNCC_AGRT5 1 14.1 428 1 SNLC_MOUSE 11 7 14.1 428 1 SNCC_AGRT5 1 1 14.1 428 1 SNCC_AGRT5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

104 AA.

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MEDLINE=1396115; PubMed=11481438; Krop I.E., Sgroi D., Porter D.A., Lunetta K.L., LeVangie R., Seth P., Kaolin C.M., Rhei E., Bosenberg M., Schnitt S., Marks J.R., Pagon Z., Bellin D., Razumovic J., Polyak K.; "HIN-1, a putative cytokine highly expressed in normal but not cancerous mammary epithelial cells."; Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).
                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in normal-1) (Secretoglobin family 3A member 1).
                                                                                                                                                                                                   Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
MEDLINE=21539178; PubMed=11682631;
Niimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
                        STANDARD;
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kimura S.;
                        MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                     MEDLINE=21396515; PubMed=11481438; Krop I.E., Serol D., Portex D.A., Lunetta K.L., LeVangie R., Seth P., Kaclin C.M., Rhei E., Boenberg M., Schnitt S., Marks J.R., Pagon Z., Belina D., Razumovic J., Polyak K., "HINT., a putative oytokine highly expressed in normal but not cancerous mammary epithelial cells."; Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001). OS \( V \) \(
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                                      Q96QR1; Q96PL0;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last amotation update)
28-FBB-2003 (Rel. 41, Last amotation update)
128-FBB-2003 (Rel. 41, Last amotation update)
28-FBB-2003 (Rel. 41, Last amotation update)
28-FBB-2003 (Rel. 41, Last amotation update)
28-FBB-2003 (Rel. 41) (Recretoglobin family 3A member 1)
38-FBB-2003 (Right of HINI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=21539178; PubMed=11682631;
Niimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
Kimura S.;
                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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R -> A (IN REF. 2).
1083873C8FAE8015 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.0%; Score 497; DB 1; Length 104; 99.0%; Pred. No. 7.2e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO, GO:005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005127; F:cytokine activity; NAS.
GO; GO:0005127; P:regulative regulation of cell growth; NAS.
Cytokine; Signal.
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                            AA.
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                            104
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EMBL; AF313458; AAL26217.1; -.
Genew; HGNC:18384; SCGB3A1.
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21 104 UT
19 19 R
104 AA; 10185 MW;
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                                                                                                                                                                                                                                                                      NCBI TaxID=9606;
                                                                                                                                                                                                            Homo sapiens
                            HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKL-AALLGLCVALSCSSAAAFLVGS-AKPVAQPVAALESAAEAGAGTLAN-PLGTLNPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Gaps
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Utercoglobin-related protein 1 precursor (Secretoglobin family 3A scGB3A2 OR UGRP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 KLLLSSLGIPVNHLIEGSOKCVAELGPQAVGAVKALKALLGALTVFG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFILASMGIPLDPLIEGSRKCVTELGPBAVGAV---KSLLGVLTMFG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 57.0%; Pred. No. 8.2e-16; Length 104; 51; Conservative 14; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL 1 21 POTENTIAL.
CHAIN 22 104 UTEROGLOBIN-RELATED PROTEIN 2.
SEQUENCE 104 AA; 10591 MM; D62F0E601FB57A6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 AA
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF311456; AAL26216.1; -. MGD; MGI: 1915912; Scgb3al. Cytokine; Signal. 21 PO SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UGR1 HUMAN
AC Q96F1;
DT 28-FEB-2003
DT 28-FEB-2003
DT 10-OCT-2003
DE Uteroglobin-;
GN SCGB3A2 OR UV
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LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104 LSSLGIPVNHLIEGSOKCVAELGPOAVGAVKALKALLGALTVFG 104

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ð 엄 ð RESULT 2

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Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                              0920H1; Q920H2; Q920H3; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Uteroglobin-related protein 1 precursor (Secretoglobin family 3A
                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS A; B AND C)
                                                                                                           member 2).
SCGB3A2 OR UGRP1
                                                                                                                                                                                                                                                                              Kimura S.;
                    MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
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      RISUBE-1018957; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Marusina M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Rokana R.J., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huly S.J., A. Pange C., Hale S., Garcia A.M., Gay L.J., Huly S.J., Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., S.M., Walledn A., Young A.C., Shevchenko Y., Bouffard G.G., A. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Rodrigues S., Schein J.E., Jones S.J.M., Marra M.A., Salska U., Schmutz J., Myers R.M., Schein J.E., Jones S.J.M., Marra M.A., Stalska U., Smills D.E., Grenztield Y.S.M., Kzzywinski M.I., Skalska U., Smills D.E., The C. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

- SUBUELLILAR LOCATION: Secreted.
- SUBUELLILAR LOCATION: Secreted.
- STMILARITY: Belongs to the uteroglobin family, UGRP subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF313455; AAL16215.1; -.
EMBL, BC024232; AAH46232.1; -.
Genew; HGNC:18391; SCGB3A2.
                                                                                                                            Kimura S.;
"UGRPI, a uteroglobin/clara cell secretory protein-related protein, is a novel lung-enriched downstream target gene for the T/BBF/NKX2.1 homeodomain transcription factor.";
Mol. Endocrinol. 15:2021-2036(2001).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                SEQUENCE FROM N.A.
MEDLINE-21539178; PubMed=11682631;
Nimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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UTEROGLOBIN-RELATED PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.9%; Score 160; DB 1; Length 93; 43.6%; Pred. No. 8.1e-08; tive 9; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FBD4BFAC2BF33718 CRC64;
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22 93
93 AA; 10161 MW;
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 606531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF214959; AAL25708 1; --
EMBL; AF274960; AAL25709 1; --
EMBL; AF274960; AAL25709 1; --
EMBL; AF274960; AAL25709 1; --
MCD; MCJ; MCJ; AF274961; AAL25710 1; --
MCD; MCJ; MCJ; SCQD3a2.
GO; GO; GO; GO; SCGST5; C: extracellular; IDA.
GO; GO; GO; SCST5; F; protein binding; IPI.
InterPro; IPR066038; Uteroglobin_supf.
PF01099; Uteroglobin; 1.
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VSVLFIPMICAYPROSKKQTFAFIERVFEGSKL -> EALS
HIV (in isoform B).
FYIId-VSP_066726.
VIIICSY -> EALSHLV (in isoform A).
FYIId=VSP_066727.
Missing (in isoform A).
                                                                                       ;
B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Indels 10; Gaps
                                                                             ISOId=0920H1-3; Sequence=VSP 006726;
-!- TISSUE SPECIFICITY: Highly expressed in lung.
-!- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
TISSUE=Lung;
MEDLINE=21539178; PubMed=11682631;
Nilmi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.9%; Score 135; DB 1; Length 139; 35.1%; Pred. No. 2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTIG=VSP 006728.
139 AA; 15431 MW; 8A2FB08ŪB41E65E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                   IsoId=Q920H1-2; Sequence=VSP_006727, VSP_006728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2e-05
17; Mismatches
                                                                                                                                                                                                                                                                                                        IsoId=Q920H1-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 35.1 nes 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92
                                                                                                                                                                                                                                                                                                                                 Name=A;
                                                                                                                                                                                                                                                                                    Name=C;
                                                                                                                                                                                                                                                                                                                                                                              Name=B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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1 MKLAALLGLCVALSCS-SAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKL

60 LLSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGAL 100

g ò RESULT 4

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-!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION.
MEDLINE-99454782; PubMed=10523501;
Smith S., de Lange T.;
Cell cycle dependent localization of the telomeric PARP, tankyrase, to nuclear pore complexes and centrosomes.";
U. Cell Sci. 112:3649-3656(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21602874; PubMed=11739745;
Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
"Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20556282; PubMed=10988299; Chi N.-W., Lodish H.F.; "Tankyrase is a Golgi-associated mitogen-activated protein kinase substrate that interacts with IRAP in GLUT4 vesicles."; J. Biol. Chem. 275:38437-38444 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Testis;
MEDLINE=99040105, PubMed=9822378;
Smith S., Giriat I., Schmitt A., de Lange T.;
"Tankyrase, a poly(ADP-ribose) polymerase at human telomeres.";
Science 282:1484-1487(1998).
                                                                                                                                                                          TWK1 HUMAN STANDARD; PRT; 1327 AA.
095271; 095272;
28-FEB-2003 [Rel. 41, Created)
10-OCT-2003 [Rel. 42, Last annotation update)
10-OCT-2003 [Rel. 42, Last annotation update)
1ankyrase I [EC 2.4.2.30] (TANKI) [Tankyrase I) (TRKS-I) interacting ankyrin-related ADP-ribose polymerase).
HOMD Saplens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND MUTAGENESIS OF HIS-1184 AND GLU-1291.
                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing, Named isoforms=2;
PTM: ADP-ribosylated (-auto).
SIMILARITY: Belongs to the PARP family.
SIMILARITY: Contains 15 ANK repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isoid=095271-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION, AND PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R GO; GO:0000781; C:chromosome, telomeric region; IDA.
R GO; GO:0000781; C:chromosome, telomeric region; IDA.
R GO; GO:0000781; F:NAD ADP-ribosyltransferase activity; IDA.
R GO; GO:0007004; P:protein binding; IPI.
R GO; GO:0007004; P:telomerase-dependent telomere maintenance; NAS.
R InterPro; IPR001660; SAM.
R InterPro; IPR001660; SAM.
R Pfam; PF00023; anh; 19.
R PR00111; ANKTARIN.
R RNART; SW00248; ANK RPRATI.
R RNART; SW00248; ANK RPRATI.
R RNART; SW00248; ANK RPRATI.
R RNART; SW00249; ANK REPEAT; 15.
R RNART; SW00249; ANK REPEAT; A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.5%; Score 83; DB 1; Length 1327;
30.5%; Pred. No. 6.5;
tive 13; Mismatches 43; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E->A: LOSS OF ACTIVITY; WHEN ASSOCIATED WITH A-1184.
MW; E14DE985C710B957 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST -> GHS (in isoform 2)
/FTId=VSP_004538.
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POLY-HIS.
POLY-PRO.
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POLY-SER.
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SAM.
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EMBL, AF082556; AAC79842.1; --
EMBL, AF082558; AAC79843.1; --
EMBL, AF082559; AAC79844.1; --
EMSP, QO0420; LAWC.
Genew; HGN:11941; TNKS.
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coelicolor 33(2).";
Nature 417:141-147(2002).
-!- CATALYTIC ACTIVITY: Anthranilate + phosphoribosyldiphosphate =
N-5'-phosphoribosyl-anthranilate + diphosphate.
-!- PATHMAY: Tryptophan blosynthesis; second step.
-!- PATHMAY: Belongs to the anthranilate phosphoribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=A3(2) / M45;
STRAIN=A3(2) / M45;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Thomson N.R., Janes K.P., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                            30-May-2000 (Rel. 39, Created)
30-May-2000 (Rel. 39, Last sequence update)
30-May-2000 (Rel. 39, Last amortation update)
Anthranilate phosphoribosyltransferase 2 (EC 2.4.2.18).
TRPD2 OR SCO3212 OR.SCEB.05C.
Streptomyces coelicolor.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP, ME 002113 - 1.

InterPro; IPR005940; Ant phspho trans.

InterPro; IPR005340; All phspho trans.

InterPro; IPR005312; Glyco trans 3.

Pfam; PF005815; Glycos trans 3.

Pfam; PF00591; Glycos trans 3.

IGRPAMs; Pf001845; Trans 4.

ITGRPAMs; TIGR01245; Trans 5.

Tryptophan biosynthesis; Transferase; Glycosyltransferase; Complete proteon.

Complete proteon.

Sand As., 34536 MW; 2706194E400B2F0D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomycineae; Streptomycetaceae; Streptomyces
70 HLIEGSQ----KCVAELGPQAVGAVKALKALLGAL 100
                                                                  149 SLAESPEAAGVSSTAPLGPGAAGPGTGVPAVSGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 LKLLLSSLGIPVNHLIEGSQKCVAELG 83
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                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 49179;

X MEDLINE=98101471; PubMed=9440521;

A REDLINE=98101471; PubMed=9440521;

Bayle D., Waengler S., Weitzenegger T., Steinhilber W., Volz J.,

Brzybylski M., Schaefer K.P., Sachs G., Melchers K.;

T Przybylski M., Schaefer K.P., Sachs G., Melchers K.;

T Przybylski M., Schaefer K.P., Sachs G., Melchers K.;

T Przybylski M., Schaefer K.P., Sachs G., Melchers K.;

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T Przybylski M., Schaefer K.P., Sachs G., Melchers K., Melche
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                   Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=214;
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Copper-transporting ATPase (BC 3.6.3.4).
732 AA.
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DIREPPO, IPRO06403, ATPRAGE-IBL CU.
INTERPO, IPRO06416, ATPRAGE-IBL TO.
INTERPO, IPRO01751, ATPRAGE IB-EV.
INTERPO, IPRO01751, ATPRAGE IB-EV.
INTERPO, IPRO01756, CU. ATPRAGE.
INTERPO, IPRO01751, ATPRAGE.
INTERPO, IPRO01751, HARVING LYAINSPL.
INTERPO, IPRO0121, HARVING LYAINSPL.
INTERPORT, IPRO0181, HYAINSE.
PERMY PRO0102; B1-EZ ATPRAGE, I.
PERMYS, PRO0102; B1-EZ ATPRAGE, I.
PRINTS, PRO01019, CATATPASE.
PRINTS, PRO01019, CATATPASE.
PRINTS, PRO01019, CATATPASE.
TIGREAMS, TIGRO1551, ATPRAGE-IB TO, I.
TIGREAMS, TIGRO1551, ATPRAGE IB TO, I.
TIGREAMS, TIGRO1551, ATPRAGE IB TO, I.
PROSITE; PSO0164; MARA, I.
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                                                                                                                                                                                                          Helicobacter felis.
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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112 LVELGDLVVSLTECSAHAAYLAAVATPGAQPAQPGLVDRYRVTRCRHEVEQGCAVLRATP 171
                                                                                                      MOUSE
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                                                                                                                                                                                                                            447 LLTLCASLEAQSEHVIAKGIVAHAKEQGIALQEVQEVQAKPGFGIKGVVGDQIIKAGNLE 506
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                                                                                                                                                                                                                                                46 --TLANPLGTLNPLKLLLSS----LGIPV--NHLIEGSQKCVAELGPQAVGA-----
                                                                                                                                                                                                        6 LLGLCVALSCSSAAAFLVGSAKPVAQPVAAL----ESAAEAGAG---------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Retina;
MEDLINE=21145589; PubMed=11247670;
Whines M.E., Lee L., Katari M.S., Zhang L., DeRossi C., Shi Y.,
Wines M.E., Lee L., McCombie W.R., Holdener B.C.;
Perkins S., Feldman M., McCombie W.R., Holdener B.C.;
"Identification of mesoderm development (mesd) candidate genes loomparative mapping and genome sequence analysis.";
Genomics 72:88-98(2001).
-!- SIMILARITY: SOME, TO TALIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33; Indels 12;
                                                                                                                                                                                   42;
                                                                       HMA.
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.9%; Score 75; DB 1; Length 362; 35.4%; Pred. No. 11; ive 6; Mismatches 33; Indels
                                                                                                                                                            Score 76; DB 1; Length 732;
Pred. No. 16;
                                                                                                                                                                       ; Pred. No. 16;
17; Mismatches 39; Indels
                                                                                           COPPER (POTENTIAL).

COPPER (POTENTIAL).

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).
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                                        EXTRACELLULAR (POTENTIAL)
                                                   POTENTIAL.
CYTOPLASMIC (POTENTIAL).
        POTENTIAL. CYTOPLASMIC (POTENTIAL).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
MESOGETM development candidate 1.
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                                                                                                                                         78853 MW;
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26.3%;
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                                                                                                                                                                                                                                                                                               ----VKALKALLG 98
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                                                                                                                                                                                     35; Conservative
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                613
732 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                          Similarity
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                                                                                    421
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09H1K6;
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3 LAALLGLCVALS-CSSAAAFLVGSAKDVAQP------VAALESAAEAGAGTL-ANP 50

Matches

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RA STAURDER R. L. Feingold E.A., Grouse L.H., Derge J.G.,

RA Altachul S.F., Zeeberg B., Bragner L., Schaemen C.M., Schuler G.D.,

Altachul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,

Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Haith F.,

A platchen M., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.E., Scheetz T.E.,

Raha S.S., Loquallano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carnhnci P., Prange C.,

Raha S.S., Loquallano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wachan P.J., McFerran K.J., Malek J.A., Gunararne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A rillalon D.K., Muzny D.W., Schergen E.J., Lu X., Gibbs R.A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butteffield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Broc. Natl Acad. Sci. U.S.A. 99:16899-16903(2002).

1- TISSUE SPECIFICITY: Ubjquitous.

21 - STMILARITY: SOMB, TO TALIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAALLGLCVALS-CSSAAAFLVGSAKPVAQP------VAALESAAEAGAGTL-ANP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryotti, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=129/SvJ;
MEDLINE=21145589; PubMed=11247670;
MEDLINE=21145589; PubMed=11247670;
Wines M.E., Lee L., Katari M.S., Zhang L., DeRossi C., Shi Y.,
Perkins S., Feldman M., McCombie W.R., Holdener B.C.;
Midentification of mesoderm development (mesd) candidate genes by
comparative mapping and genome sequence analysis.";
Genomics 72:88-98(2001).
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                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Megoderm development candidate 1.
                                                                                                                                                                                                                                                                                     362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                             172 LADMTPOLLLEVSQGLSRN 190
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LGTLNPLKLLLSSLGIPVN 69
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Conservative
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nes 28; Conserv
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01-NOV'1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Probable serine/threonine protein kinase SNF1LK (EC 2.7.1.-) (HRT-20)
(Myocardial SNF1-like kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND REVISIONS TO 8; 16-18; 44-45; 316 AND 435.
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R HSSP; P24941; 1AQ1

R MGD; MG1:104774; Snfilk.

R InterPro; IPR008271; Ser_thr_pkin_AS.

InterPro; IPR008271; Ser_thr_pkinase.

R InterPro; IPR00129; Tyr pkinase.

R InterPro; IPR00149; UBA_domain.

R FRINTS; PR00109; TYRKIAASE.

R SWART; SMO0109; TYRKIAASE.

R PROSITE; PS00101; PROTEIN KINASE ATP; 1.

R PROSITE; PS00101; PROTEIN KINASE DOM; 1.

PROSITE; PS00101; PROTEIN KINASE DOM; 1.

R PROSITE; PS00101; PROTEIN KINASE DOM; 1.

R PROSITE; PS00101; DROTEIN KINASE DOM; 1.

R PROSITE; PS00101; DROTEIN KINASE DOM; 1.

R DOMAIN 303 343 UBA.

T DOMAIN 303 341 ATP (BY SIMILARITY).

T BINDING 56 56 ATP (BY SIMILARITY).

T SEQUENCE 779 AA; 85027 MW; 7808131BC46D9C4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruiz J.C.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-435 FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                    779 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subfamily.
-!- SIMILARITY: Contains 1 UBA domain.
                                                                                                                                             172 LADMTPQLLLEVSQGLSRN 190
                                                                                     51 LGTLNPLKLLLSSLGIPVN 69
                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Embryo;
                                                                                                                                                                                                                                                                                    SNIL MOUSE
Q60670;
                                                                                                                                                                                                                            RESULT 10
SN1L_MOUSE
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                                                                                                                         .
ب
                                                                                                                                                                                                                                                                                                                10 CVALSCSSAAAFLVGSAKPVAOPVAALESAAEAGAGTLANP--LGTLNPLKLLLSSLGIP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the endocellular obligate symbiont of tsetse files, Wigglesworthia glossinidia.";
Nat. Genet. 32:402-407(2002).

-i- FUNCTION: Catalyzes the acyloin condensation reaction between C atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield 1-deoxy.D-xylulose-5-phosphate (DXP) (By similarity).

-i- CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = 1-deoxy.D-xylulose 5-phosphate + CO(2).

-i- CAFACTOR: Binds 1 thiamine pyrophosphate per subunit (By similarity).

-i- COFACTOR: Binds 1 thiamine pyrophosphate per subunit (By similarity).

-i- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway, first step.

-i- PATHWAY: Biosynthetic pathway to thiamine and pyridoxol; first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=22297718; PubMed=12219091;
Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
Aksoy S.;
14.7%; Score 74; DB 1; Length 779; 32.9%; Pred. No. 26; ive 11; Mismatches 30; Indels 12; Gaps

    -1- SUBŪNIT: Homodimer (By similarity).
    -1- SIMILARITY: Belongs to the transketolase family. DXPS subfamily.

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R HAMAP; MF 00315; -; 1.

R InterPro; IPR00547; Dransketo C like.

R InterPro; IPR005476; Transketolase_C.

R InterPro; IPR005474; Transketolase_C.

R InterPro; IPR005474; Transketolase_C.

R InterPro; IPR005474; Transketolase_N.

R Pfam; PF02779; transket_Dyr; 1.

R Pfam; PF02779; Transketolase_C; 1.

R PG3ITE; PS00801; TRANSKETOLASE_I; 1.

R PROSITE; PS00802; TRANSKETOLASE_I; COMPLETE PS00802; TRANSKETOLASE_I; COMPLETE PS00802; TRANSKETOLASE_I; COMPLETE PS00802; TRANSKETOLASE_I PS00802; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wigglesworthia glossinidia brevipalpis.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Wigglesworthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.6%; Score 73.5; DB 1; Length 626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
11-deoxyxyD-xylulose 5-phosphate synthase (EC 2.2.1.7) (1-deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         626 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GŚŚSATPVLOTOA 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 VNHLIEGSOKCVAELGPQA 86
                  Query Match
Best Local Similarity 32.94
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Q8D357;
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R -> K (IN REF. 2). ; 7BF745AF28F17E6E CRC64;

84908 MW;

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776 AA;
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NCBI_TaxID=274;
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CONFLICT
                                                                                                                                                                                                                                                                                            546
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                                                                                              22 LVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNHLIEGSQKCV-A 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
--- SMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
subfamily.
--- SIMILARITY: Contains 1 UBA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Feldman J.D., Vician L., Crispino M., Hoe W., Baudry M., Herschman H.R.; Herschman H.R.; The Kidz gene encodes a protein kinase induced by depolarization in "The Kidz gene encodes a protein kinase induced by depolarization in
                                                                                                                                                                                                                                                                                                                    SNIL RAT STANDARD; PRT; 776 AA.

SNIL RAT (9R081; 09R081; 16-0CT-2001 (Rel. 40, Last sequence update)

16-0CT-2001 (Rel. 42, Last annotation update)

10-0CT-2003 (Rel. 42, Last annotation update)

inducible serine/threonine protein kinase SNF1LK (EC 2.7.1.-) (Salt-inducible protein kinase) (Protein kinase KID2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Sprague Dawley, TISSUE-Adrenal gland, MEDLINE=99330184; PubMed=10403390; Wang Z., Takemori H., Halder S.K., Nonaka Y., Okamoto M.; Wang Z., Takemori H., Halder S.K., Nonaka Y., Okamoto M.; Cloning of a novel kinase (SIK) of the SNF1/AMPK family from high salt diet-treated rat adrenal."; FEBS Lett. 453:135-139(1999).
                          1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 threonine-protein kinase; ATP-binding
                          41; Indels
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ATP (BY SIMILARITY)
BY SIMILARITY.
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    30.0%; Pred. No. 24; ive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB020480; BAA82673.1; -.
EMBL; AF106937; AAF14191.1; -.
HSSP; P24941; 1AQ1.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser Lhr Dkin AS.
InterPro; IPR008290; Ser Lhr Dkin AS.
InterPro; IPR00449; UBA domain.
                                                                                                                                                          81 ELGPQAVGAVKALKALLGAL 100
                                                                                                                                                                                            24; Conservative
    Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                   SN1L RAT
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                                                                                                                                                 6 LLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLSSLG 65
                                                                                                           10 CVALSCSSAAAFLVGSAKPVAQPVAALESAABAGAGTLANP--LGTLNPLKLLLSSLGIP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y08333; CAA69650.1; -.
HAMAP; MF_00036; -; 1.
InterPro; IPR003136; DHHAL:
InterPro; IPR003139; tRNA-synt_2c.
InterPro; IPR006193; tRNA-synt_Ala.
Pfam; PF02272; DHHAL: 1.
Pfam; PF01411; tRNA-synt_Ala.
FANN: PR00980; TRNA-SYNTHALA.
TIGREAMS; TIGR00344; ala6; 1.
PR003TR3; PS0860; AM TRNA_INALIASE II ALA; 1.
PR003TR3; PS0860; AM TRNA_INALIASE II ALA; 1.
RR05TR3; PS0860; AM TRNA_INALIASE II ALA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                э;
                                                              13;
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Ouery Match
Best Local Similarity 33.7%; Pred. No. 28;
Matches 28; Conservative 11; Mismatches 31; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                          882 AA.
                                                                                                                                                                                                                                                                                 -----GŚÓSATPVLOSOAGLGA 562
                                                                                                                                                                                                                            68 VNHLIEGSQKCVAELGPQA-VGA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 32.0.,
Local 30, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermus thermophilus.
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Ligase; T. SEQUENCE

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397 AA.

PRT;

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE 2160851; Pubmed=11743194; Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flansgan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.; Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens (58."; Science 234:232-2328(2001).
-!- CATALIXIC ACTIVITY: ATP + succinate + COA = ADP + succinyl-COA +
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIJUNE=2160856); PubMed=11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Dacatherage G., Gillet W., Grant C., Kuryavin T., Levy R. Li M.-J., McClelland E., Palmieri A., Raymond C.; Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : E.W.; genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
-!- SIMILARITY: Belongs to the succinate/malate CoA ligase beta
subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphate.
-!- PATHWAY: Tricarboxylic acid cycle.
-!- SUBUNIT: Composed of an alpha chain and a beta chain (By
                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last sequence update)
50-CCT-2003 (Rel. 42, Last annotation update)
50-CCT-2003 (Rel. 42, Last entotation update)
50-CC OR ATU2638 OR AGR_C_4780.
50-CC OR ATU2638 OR AGR_C_4780.
63-CC OR ATU2638 OR AGR_C_4780.
64-CC OR ATU2638 OR AGR_C_4780.
65-CC OR AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AE009211; AAL43619.1; -. EMBL, AE00817; AK88359.1; -. PIR, AE2900; AE2900. BIR; F97675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=176299;
LT 14
AGRTS
SUCC AGRTS
QSUCE0;
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                                                                                                                                           16
                                                                                                                                                                             57
                                                                                                                                         18 AAAFLVGSAKPVAQPVAALE-SAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNHLIEGSO
                                                                                                                                                                             8 AKALLKGYGAPVAEGVAILKVEEAEAAKQLPGPLYV---VKSQIHAGG------RGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-97014266; PubMed-8861101;
Kaestner K.H., Schuetz G., Monaghan A.P.;
"Expression of the winged helix genes fkh-4 and fkh-5 defines domains in the central nervous system.";
Mech. Dev. 55:221-230(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93361500; PubMed=7689224;
Kaestner K.H., Lee K.H., Schloendorff J., Hiemisch H.,
Monadhan A.P., Schuetz G.;
Monadhan A.P., Schuetz G.;
Six members of the mouse forkhead gene family are developmentally regulated.";
Proc. Natl. Acad. Sci. U.S.A. 90:7628-7631(1993).
-: SUBCELLULAR LOCATION: Nuclear.
-: DEVELOPMENTAL STRAES: Expressed during embryogenesis.
-: SIMILARITY: Contains 1 fork-head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R EMBL; X1942; CAR053393-1; -.
R EMBL; X71942; CAA60744.1; -.
R PIR; D47746; D47746.
R HSSP, Q6312545; 24FH.
R HSSP, Q631347468; Foxb.
R InterPro; IPR001766; TF Fork_head.
R InterPro; IPR001766; TF Fork_head.
R ProDom; PR00053; FORKHAAD.
R ProDom; PR00039; FH; T. RFOrk_head; 1.
R PROSITE; PS00658; FORK_HEAD.1; 1.
R PROSITE; PS00658; FORK_HEAD.1; 1.
R PROSITE; PS00658; FORK_HEAD.2; 1.
R PROSITE; PS00658; FORK_HEAD.3; 1.
R PROSITE; PS00658; FORK_HEAD.3; 1.
R PROSITE; PS00658; FORK_HEAD.3; 1.
R PROSITE; PS00139; FORK_HEAD.3; 1.
R PROSITE; PS00139; FORK_HEAD.3; 1.
R DNA_BIND.
I 10 3 FORK-HEAD.
                                                       Query Match
Best Local Similarity 36.2%; Pred. No. 21;
Matches 29; Conservative 8; Mismatches 31; Indels
Tricarboxylic acid cycle; Complete proteome.
E 397 AA; 41899 MW; 223C1A3825764F9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAX-2000 (Rel. 39, Last annotation update)
Forkhead box protein B2 (Transcription factor FKH-4).
FOXE2 OR FKH4.
                                                                                                                                                                                                                                                                                                                                                                 428 AA
                                                                                                                                                                                                                                                            58 K-FKELGPDAKGGVRLAKSI 76
                                                                                                                                                                                                                        77 KCVAELGPQAVGAVKALKAL 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X92591; CAA63335.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 4-114 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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A MEDLINE=103-6507; PubMed=11481430;
A Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
A Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
A Capela D., Barloy-Hubler F., Gouzy J., Cadiou E., Dreamo S., Gloux S.,
A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Pohl T., Portetalle D., Puncher A., Purnelle B., Ramsperger U.,
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
A Ranalysis of the chromosome sequence of the legume symbiont
Sinorbizobium meliloti strain 1021.";
Froc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
I. Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
C. chromosomal replication Binds to the origin of replication; it binds specifically double-stranded DNA at a 9 bp consensus (dnaA box): S'-TTATC(C/A)A(C/A)A-3'. DnaA binds to ATP and to acidic phospholipids.
C. -: SIMILARITY: Belongs to the dnaA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                           11 VALSCSSAAAFLVGSAKPVAQ-PVAALESAAEAGAGTLANPLGTINPL-----KL 59
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                          60 LLSSLGIP----VNHL---IEGS-QKCVAELGPQAVGAVKALKALLGALTVFG 104
                                                                                                                                                                                                                                                                                                                                     280 VLQAGGLPLASVMHHLGYPVPGQLSNVVGSVWPH-VGVMDSVAAAAAAAAAAG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Margolin W., Bramhill D., Long S.R.; "The dnaA gene of Rhizobium meliloti lies within an unusual gene
                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-070-1994 (Rel. 29, Created)
16-077-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
28-FEB-2003 (Rel. 41, Last amnotation update)
DNAA OR R00368 OR SWC01167.
DNAA OR R00368 OR SWC01167.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobianes, Shnorhizobium/Ensifer group, Sinorhizobium.
                                                                                                                                                            14.1%; Score 71; DB 1; Length 428; 29.2%; Pred. No. 28; ative 17; Mismatches 43; Indels
                                                                                                                             DB8A8EFD1E94AB10 CRC64;
POLY-HIS.
POLY-HIS.
POLY-PRO.
POLY-ALA.
POLY-ALA.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 125439; AAA26258.1; ALT INIT.
EMBL; 1.32265; AAA91097.1; ALT INIT.
EMBL; ALS91783; CAC41805.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rangement.";
Bacteriol. 177:2892-2900(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95270610; PubMed=7751302;
 139 153 POL
156 162 POL
163 162 POL
217 231 POL
249 258 POL
341 330 POL
396 399 POL
428 AA, 45170 MW, D
                                                                                                                                                                                                     33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=382;
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P35890;
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                                                                                                                                 SEQUENCE
                                                                                                                                                                  Query Match
Best Local
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Matches
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XX MEDLINE-2168199; PubMed=11823852;

ARBITINE-2168199; PubMed=11823852;

ARBITINE-2168199; PubMed=11823852;

ARIAL M., Genin S., Artiguenave F., Gauzy J., Mangenot S.,

Arlat M., Claudel Renard C., Cuntolico L.,

Arlat M., Claudel Renard C., Cunton W., Demange N.,

A Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,

Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,

A Reisenbach J., Boucher C.A.;

Reisenbach J., Boucher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

"Nature 415:497-502(2002).

-I-FUNCTION: Seems to be the binding site for several of the factors involved in protein synthesis and appears to be essential for accurate translation (By similarity).

-I-SIMILARITY: Belongs to the Li2P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 AFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNHLIE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ъ
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
HAMAP; MF_00377; -; 1.
InterPro: IPR001593; AAA ATPase.
InterPro: IPR001593; BAC_DnaA.
PEAM; PR00308; bac_dnaA; 1.
PEAM; PR00051; DNAA.
SWART; SM00382; AAA; 1.
PROSITE; PS01009; DNAA; 1.
DNA replication; DNAA; 1.
NNA replication; DNAAbinding; ATP-binding; Complete proteome.
NP BIND 181 188
ATP (POTENTIAL).
SEĞUENCE 480 AA; 53579 MW; A346219945FAD6A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                             14.1%; Score 71; DB 1; Length 480; 38.9%; Pred. No. 31; ative 11; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probon; PD001226; Ribosomal L12; 1.
Probon; PD001226; Ribosomal L12; 1.
TIGRPAMS; TIGNO0855; L12; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 124 AA; 12520 MW; 271C3CF71F80269E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
50s ribosomal protein L7/L12.
RPLL OR RSC3035 OR RS04722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AL646073; CAD16744.1; -.
HAMAP, MF 00368; -; 1.
InterPro; IPR008932; Ribos L12/7 olig.
InterPro; IPR00206; Ribosomal L12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 38.9%, ses 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28; Conservative
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Best Local Similarity
Matches 28; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEOUENCE FROM N.A.
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28-FEB-2003
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Q8XÜZ7;
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Matches
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RESULT 17
REALSO
DT 28-FE
DT 
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234 RVAAVSGIPTVLTCASNAGPAMMGDPVGTVFAPVKARGSSRRLWIGFAADPRGTIVVDAG 293

...--NPLKLLLS-----SLGIPV-----NHLIEGSQKCVAELGPQAVGAVK 91

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SSAAAFLVGSAKPVAOPVAALESAAEA---GAGTLANPLGTLNPLKLLLSSLGI-PVNHL 71
                                                      34 SAAAVAVAGPAGGAAAPAAEEKTEFDVILKGAG--ANKVGVIKAVR-EITGLGLKEAKDL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The genome sequence of Biidobacterium longum reflects its adaptation to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).
-!- FONGTION: Catalyzes the transfer of a phosphate group to glutamate to form glutamate 5-phosphate which rapidly cyclizes to 5-
oxoproline.
-!- CATALYTIC ACTIVITY: ATP + L-glutamate = ADP + L-glutamate 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 28.1%; Pred. No. 42;
Matches 36; Conservative 13; Mismatches 48; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REMEL, AE014755, AAN25086.1, ...
REMAAP, MF_00456. -; 1.
RICAPTO: IPR001048; Aa kinase.
RICAPTO: IPR001057; Glu 5kinase.
RICAPTO: IPR0010575; ProB.
RICAPTO: IPR0010575; ProB.
RICAPTO: IPR0010575; ProB.
RICAPTO: IPR0010575; ProB.
REMINITS; PR004747; ProB.; 1.
REMART: SM00559; Pub.; 1.
REMART: REMARTE SKINASE; 1.
REMART: PS00890; Pub.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22294977; PubMed=12381787;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
Peessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
Pridmore R.D., Arigoni F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphate.
-- PATHWAY: Proline biosynthesis; first step.
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: Belongs to the glutamate 5-Kinase family.
--- SIMILARITY: Contains 1 PUA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 377 AA; 39187 MW; 2196B4E8563223FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 AA
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                                                                                                                                                                                 72 IEGSOKCVAELGPOAVGAVKALKALLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROB BIFLO
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PROB_BIFLO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N SEQUENCE FROM N.A.

Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,

Chung E., Allen E., Araujo R., Kalman S., Komp C., Kurdi O., Lew H.,

A Lin D., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;

L Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

C. - FUNCTION: PART OF THE BINDING-PROTEIN-DEPRYDENT TRANSPORT SYSTEM

CC TRANSLOCATION OF THE SINDING-PROTEIN PROBABLY RESPONSIBLE FOR THE

TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.

CC -: SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.

CC -: INDUCTION: Controlled in part by the amount of available iron.

CC -: SIMILARITY: Belongs to the binding-protein-dependent transport

CC -: SIMILARITY: Belongs to the binding-protein-dependent transport

System permease family. FecCD subfamily.
294 AGQAIRGGRASLLAAGALEVHGDFSAGDPVWIDAESGEHLARGLAGFDSEEIPQMLGRNT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shea C.M., McIntosh M.A., "Nucleotide sequence and genetic organization of the ferric enterobactin transport systems in monology to other periplasmic binding protein-dependent systems in Escherichia coli."; Mol. Microbiol. 5:1415-1428(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chenault S.S., Earhart C.F.; "Construction of the Escherichia coli ferrienterobactin permease."; Mol. Microbiol. 5:1405-1413(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=K12 / M01655;
MEDLINE=97426617, PubMed=9278503;
MEDLINE=97426617, PubMett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                 FEDD ECOLI STANDARD; PRT; 334 AA.
FEDD ECOLI STANDARD;
01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1991 (Rel. 41, Last annotation update)
FEDD OR BOS90.
FEDD OR BOS90.
FEDD OR BACHETIA; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=K12;
MEDLINE=92157868; PubMed=1838574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=K12;
MEDLINE=92157867; PubMed=1787794;
                                                                                          354 AOLKRFLG 361
                                                  92 A-LKALLG 98
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5, 54

2 KLAALLGLCVALSCSSAA--AFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTL----

_ <u>:</u> ::

Tue Apr 6 07:57:55 2004

18-02-428-428-18D

This motif is involved in downmodulation of cellular responses. The phosphorylated ITIM motif binds to the SH2 domain of PTPN6/SHP-1.

> RESULT g à ANDURINE TACH. W. M. M. M. M. M. Warki A.; MEDLINE-21576254; PubMed=11579105; MEDLINE-21576254; PubMed=11579105; MEDLINE-21576254; PubMed=11579105; MEDLINE-21576254; PubMed=11579105; MEDLINE-21576254; PubMed=11579105; Medline and characterization of a novel mouse Siglec, mSiglec-F: RT differential evolution of the mouse and human (CD33) Siglec-3-related RT differential evolution of the mouse and human (CD33) Siglec-3-related RT differential evolution of the mouse and human (CD33) Siglec-3-related RT dependent binding to cells. Preferentially binds to alpha, 3-Inked sialic acid. The Sialic acid recognition site may be masked CC by.cis interactions with sialic acid recognition site may be masked CC --- SIBCELUTAR LOCATION: Type I membrane protein.
>
> CC --- SIBCELUTAR LOCATION: Type I membrane protein.
>
> CC --- TISSUE SPECIFICITY: Predominantly expressed by immature monocytes.
>
> CC --- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (TIIM). 41 LEAFSGTCQSADCTIVLDARLPRTLAGLLAGGALGLAGALMQTLTRNPLADPGLLGVNAG 100 33 ------GTUNPLKLLLSSLGIPV 68 43; Indels 58; Gaps Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. EMBL; X57471; CAA40707.1; -.
> EMBL; X59402; CAA42043.1; -.
> EMBL; X59402; CAA42043.1; -.
> EMBL; M82598; AAB40789.1; -.
> EMBL; U82598; AAB40789.1; ALT_INIT.
> PIR; S16296; EDD
> ENCOGENE; EG10296; EDD
> InterPro; IPR000515; BPD transp.
> InterPro; IPR000515; PecD.
> ProDon; PD001827; PecCD; 1.
> ProDon; PD001827; PecCD; 1.
> Iron transport; Transport; Inner membrane; Transmembrane; SILF MOUSE
>
> SILF MOUSE
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> TO SILF MOUSE
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> COSOG3:
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> SILF MOUSE
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> COSOG3:
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> SILF MOUSE
>
> SILF MOUS DB 1; Length 334; POTENTIAL. RV -> AL (IN REF. 2). BBSC5E939A96951B CRC64; 69 NHLIEGSOKCVAELGPQAVGAVKALKALLGALTV 102 Query Match 13.5%; Score 68; DB 1 Best Local Similarity 22.1%; Pred. No. 42; Matches 34; Conservative 19; Mismatches POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. 33871 MW; Iron transport; Transport Transport; Transport Transport Transport Transport 10 Transport 93 Transport 121 Transport 193 Transpo 334 AA; SEQUENCE FROM N.A. NCBI_TaxID=10090; SEQUENCE RESULT 셤 NAME OF THE PROPERTY OF THE PR g ઠે ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      447 IMALILAVCLC------LIFFTVKVLRKKSALKVAATKGNHLAKNPASTINSASITSS 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 13.5%; Score 60; DB 1; Length 569; Local Similarity 29.9%; Pred. No. 67; 18. Conservative 11; Mismatches 38; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
SIALIC ACID BINDING IG-LIKE LECTIN-F.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE 1.
IG-LIKE Q2-TYPE 2.
ITIM MOTIF.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
PTPN6/SHP-1.
-!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (sialic acid binding Ig-like lectin) family.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. .) (PC
N-LINKED (GLCNAC. .) (PC
8093838090484FCI CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein KIAA0233.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 --SLGIPV-NHLIEGSQKCVAELGPQA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61476 MW;
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AC 092508;
DT 16-0CT-2001
DT 16-0CT-2001
DT 16-OCT-2001
GN Hypothetical
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us-09-997-428-408.rsp

Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.; "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
13.4%; Score 67.5; DB 1; Length 2035;
Best Local Similarity 29.2%; Pred. No. 2.3e+02;
Matches 19; Conservative 12; Mismatches 29; Indels 5; Gaps
         SEQUENCE FROM N.A.

TISSUE=Bone marrow,

MEDILINE=91919544; PubMed=9039502,

MEDILINE=91919544; PubMed=9039502,

Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,

Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;

"Prediction of the coding sequences of unidentified human genes."

"The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced hanalysis of cDNA chones from cell line KG-1 and brain.";

DNA Res. 3:321-329(1996).
                                                                                                                                                                                                                                                                                                                                                                                                   450 453 POLY-LEU.
618 621 POLY-LEU.
940 944 POLY-GLU.
1409 1418 POLY-GLU.
1487 1490 POLY-TLE.
160 1683 POLY-LEZ.
2035 AA; 233040 MW; F337E333DFC0CBB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   POLY-GLN.
POLY-LEU.
POLY-LEU.
POLY-GLU.
POLY-GLU.
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POLY-GLU.
                                                                                                                                                                                                                                                                                                                              EMBL; D87071; BAA13240.1; -.
Hypothetical protein.
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270
621
621
1444
1683
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0 85 QAVGA 89 à

1145 REAGA 1149

(Glycoprotease). The state of the state of B129 C3_246 OR B1620_C3_226. GCP OR ML0379 OR U229E OR U1620C OR B229_C3_246 OR B1620_C3_226. Mycobacterium leprae. Bacteria; Actinobacteria; Actinobacteria; Actinobacteriaceae; Mycobacterium. Mycobacteriaceae; Mycobacterium. Mycobacteriaceae; Mycobacterium. GCP MYCLE STANDARD; PRT; 351 AA.
P37959; Q49725;
01-0CT-1994 (Rel. 30, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable O-sialoglycoprotein endopeptidase (EC 3.4.24.57)

SEQUENCE FROM N.A. Smith D.R., Robison K.; Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.

STRAIN=TN;
MEDLIKE=21128732; PubMed=11234002;.
MEDLIKE=21128732; PubMed=11234002;.
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,

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13.3%; Score 67; DB 1; Length 351;
Best Local Similarity 34.5%; Pred. No. 53;
Matches 29; Conservative 6; Mismatches 39; Indels 10; Gaps "Mycobacteria" contain two groEL genes: the second Mycobacterium leprae groEL gene is arranged in an operon with groES."; and. Microbiol. 6:1995-2007(1992).

-!- FUNCTION: Could be a metalloprotease.
-!- CATALYTIC ACTIVITY: Hydrolysis of O-sialoglycoproteins; cleaves 31-Arg-| Asp-32 bond in glycophorin A. Does not cleave unglycosylated proteins, desialylated glycoproteins or glycoproteins that are only N-glycosylated.
-!- COFACTOR: Zinc (Probable).
-!- SIMILARITY: Belongs to peptidase family M22. SEQUENCE OF 286-351 FROM N.A.
MEDLINE-22374850; PubMed-1354834;
de Wit T.P.R., Bekelie S., Osland A., Miko T.L., Hermans P.W.M.,
van Soolingen D., Drijfhout J., Schoeningh R., Janson A.A.M.,
Thole J.E.R.; REMEL; MO020; AAALT310.1; ALT_SEQ.
EMBL; ALOS3918, CAC29897.1; -.
EMBL; MO015; AAAC4326.1; -.
EMBL; WO0015; AAAC4326.1; -.
EMBL; WO0015; AAAC4326.1; -.
EMBL; WO0015; AAAC4326.1; -.
EMBL; WO0015; AAAC4326.1; -.
EMBCOPE, MOSOPS; PEPTIGASE M22.
EMBCOPE, PRESPONSOS; PEPTIGASE M22.
EMBCOPE, PRESPONSOS; PEPTIGASE M22.1.
EMBCS; PRESPONSOS; PEPTIGASE M22; 1.
EMBCSTE; PSO1016; GLYCOPROTEASE; 2.
EMBCSTER PSO1016; GLYCOPROTEASE; 2.
E METAL 128 128 ZINC (POTENTIAL). SEQUENCE 351 AA; 35405 MW; F76A14B739A7BAE4 CRC64; 64 LGIP---VNHLIEGSOKCVAELGP 84 SOLUTION SERVICE SERVI 셤 à

115 WGVPFYAVNHLGGHLAADVYEHGP 138

FESULT 23
FUNC_PSESM
ID FUNC_PSESM STANDARD; PRT; 464 AA.
AC Q88570;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last sequence of European C).
CS Bactorias Proteobacteria; Gammaproteobacteria; Pseudomonadales;
CC Bactoria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
CX NCBI_TAXID=323;

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Score 66.5;
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MEDLINE=95362824; PubMed=7635958;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.2%;
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                                                    SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                  2 KLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FFB-1994 (Rel. 28, Created)
01-FFB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Thromboxane A2 receptor (TXA2-R) (Prostanoid TP receptor) (TXR2)
                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                          SUBSTRATE CARBOXYL (POTENTIAL) 6B12FFF77257FFD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                       14; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 SGPRAGLAEVRLPANE--PGSSIMPGKVNPTOCEALSML 334
                                                                                                                                                                                                                                                                                                            Interprision 1980 1985; Fumarate lyase.
InterPro; IPR00948; L-Aspartase-like.
Edm.; PF00206; lyase 1; L-Aspartase-like.
PROMO149; FUMARATELYASE.
PROSITE; PRO0149; FUMARATE LYASES; 1.
PROSITE; PS00163; FUMARATE LYASES; 1.
Ayses; Tricarboxyllic acid cycle; Complete proteome.
ACT SITE 186 186 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 -----LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKAL 93
                                                                                                                                                                                                                                                                                                                                                                                                               68;
                                                                                                                                                                                                                                                                                                                                                                                                      13.3%; Score 67; 31.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUB-Kidney;
                              MEDLINE=22834015; PubMed=12928499;
                                                                                                                                                                                                                                                                                 EMBL; AE016862; AAO55251.1; -.
TIGR; PSPTO1731; -.
HAMAP; MF_00743; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                     49077 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                       31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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Rattus norvegicus (Rat)
                                                                                                                                                                                            Fumarase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                     464 AA;
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ACT SITE
BINDING
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Best Local S
Matches 31
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P34978;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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AC DT 01-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at kidney thromboxane receptor: molecular cloning, signal ansduction, and intrarenal expression localization."; clin. Invest. 96:657-664(1995).
                                                                                                                                                                                                                                                                                                                    STRAIN-Sprague-Dawley, TISSUE-Brain;
MEDLINE-95210358; PubMed=7696353;
Kitanaka J., Hashimoto H., Sugimoto Y., Sawada M., Negishi M.,
Suzumura A., Marunouchi T., Ichikawa A., Baba A.;
"CDNA cloning of a thromboxane A2 receptor from rat astrocytes.";
Biochim. Biophys. Acta 1265:220-223(1995).
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N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
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EMBL; D32080; BAA06644.1; -.
FIR; I55623; I55623; GPCR Rhodpsn.
InterPro; IPR008365; ProstanoidR.
Fram; PR00001; 7tm.1; 1.
FRINTS; PR01789; PROSTANOIDR.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
FROSITE; PS00262; G PROTEIN RECEP F1 1; 1.
FOSITE; PS00262; G PROTEIN RECEP F1 1; 1.
FOSITE; PS00262; G PROTEIN RECEP F1 1; 1.
FOSITE; PS00262; G PROTEIN RECEP F1 2; 1.
FORMALN.
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Length 341;

DB 1;

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                                                                                                                                                                                                                                                                                                                                                                                                                            295 AAAAAAAAAFHPHSPPPPPPPPHGAAAELARTAFGYRPHPLGAALPGPLPASAAKAGGPGA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nonspecific lipid-transfer protein D precursor (LTP D) (Wax-associated
protein 9D).
                                                                                                                                                                                                                                                                                                                                                                                        12 ALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTL--NPLKLLLSSLGIP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids; eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94263227; PubMed=8203911; Problem 1: Kolattukudy P.E.; Pyee J., Yu H., Kolattukudy P.E.; Identification of a lipid transfer protein as the major protein in the surface wax of broccoli (Brassica oleracea) leaves."; Arch. Biochem. Biophys. 311:460-468(1994).
                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                               DB 1; Length 465;
                                                                                                                                                                                                                                                                                                                                                     43; Indels
                                                                                                                                                                                                                                                                         D3E7854909CCBFAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 SALARSPFSIESIIGGS-----LGPAAAAAAAAAAA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 ------VNHLIEGSQKCVAELGPQAVGAVKALKA 95
                                                                                                                                                                                                                                                                                                           Score 66.5; DB Fred. No. 76; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 AA
                                                                                                GLY.
HEAD.
                                                                                                                                   POLY-ALA.
POLY-ALA.
POLY-PRO.
POLY-ALA.
                                                                                                                                                                                                             POLY-PRO.
POLY-ALA.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                           POLY-,
POLY-(
FORK-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica oleracea (Cauliflower).
                                                                                                                                                                                                                                                                           46140 MW;
                                                                                                                                                                                                                                                                                                                 13.2%;
28.9%;
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 28.9'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                            303
3315
434
                                                                                                                                                                                            293
309
375
428
465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IISSUE=Leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BRAOL
                                                                                                                   DOMA BIND
                                                                                                                                                                                                                   DOMAIN
DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLTD_BRA
043304;
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                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                              115 GLCPLLLGAAMAAERFVGITRPFSRPAATSRRAWATVGLVWVGAGTLG------L 163
                                                            8 GLC-VALSCSSAAAFLVGSAKPVAQPVAALESA-----AEAGAGTLANPLGTLNPLKLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95045392; PubMed=7957066;
MEDLINE-95045392; PubMed=7957066;
MEDLINE-95045392; PubMed=7957066;
Prierrou S., Hellqvist M., Sauuelseon L., Enerbaeck S., Carlsson P.;
Prierrou S., Hellqvist M., Sauuelseon L., Enerbaeck S., Carlsson P.;
Prierrou S., Hellqvist M., Bandisson D., Seven human forkhead proteins:
binding site specificity and DNA bending.";
EMBO J. 13:5002-5012(1994).
I- FUNCTION: Binding of FREAC-3 and FREAC-4 to their cognate sites results in bending of the DNA at an angle of 80-90 degrees.
-:- SUBCELLUIAR LOCATION: Nuclear.
-:- SIMILARITY: Contains 1 fork-head domain.
                                                                                                                                                                                                                                                                                              Q16676; Q12949;
Q1007-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
20-knead box protein D1 (Forkhead-related protein FXHL8) (Forkhead-related transcription factor 4) (FREAC-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ernstsson S., Pierrou S., Hulander M., Cederberg A., Hellqvist M., Carlsson P., Enerback S., Hulander M., Carlsson P., Enerback S., Forther S., Carlston P., Enerback S., Forther S., Carlston Of the human forkhead gene FREAC-4. Evidence for regulation by Wilms' tumor suppressor gene (WT-1) and p53."; J. Biol. Chem. 271:21094-21099(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                               61 LSSLGIPVNHLIEGSQKCV----ABLGPQAVGAVKALKALLGALTV 102
                       38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0003700; F:transcription factor activity; TAS. InterPro; IPR001766; TF Fork_head.
Pfam; PF00250; Fork_head; 1.
PRINTS; PR00053; FORKHEAD.
PRODOM; PD000425; TF Fork_head; 1.
PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00659; FORK_HEAD_2; 1.
PROSITE; PS00659; FORK_HEAD_2; 1.
                                                                                                                                                                                                                                                                                465 AA.
                    32; Conservative 11; Mismatches
    30.2%; Pred. No. 58;
                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=96355467; PubMed=8702877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U59832; AAC50661.1; -.
EMBL; U59831; AAC50660.1; -.
EMBL; U13222; AAA92039.1; -.
                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRANSFAC; T02472; -.
Genew; HGNC:3802; FOXD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; G02738; G02738.
PIR; S51627; S51627.
HSSP; Q63245; ZHFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601091;
                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; ]
MIM; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                             HUMAN
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Gaps

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                                                                                                                                                          4 AALLGLCVALSCSSAAAFLVG-----SAKPVAQPVAALESAAEAGAGTLA--NPL--- 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per molecule (Potential).
-:- SUBUNIT: Heterotrimer of alpha, beta and gamma subunits.
-:- SUBCELLULAR LOCATION: Periplasmic.
-:- BIOTECHNOLOGY: Has potential use in bioremediation of waste sites contaminated with chlorate, such as pulp and paper industry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJS66363; CAD97450.1; -. EMBL; Signal.
Electron transport; Periplasmic; Heme; Signal.
SIGNAL 1 27 POTENTIAL.
CHICKATE REDUCTASE GAMMA SUBUNIT.
CHAIN 28 239 CHLORATE REDUCTASE GAMMA SUBUNIT.
VETAL 174 74 IRON (HEME B AXIAL LIGAND) (POTENTIAL).
NETAL 178 IRON (HEME B AXIAL LIGAND) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A., AND CHARACTERIZATION.

Danielsson Thorell H., Stenklo K., Karlsson J., Nilsson T.;

"A gene cluster for chlorate metabolism in Ideonella dechloratans.";

Appl. Environ. Microbiol. 69:5885-5592(2003).
                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Chlorate reductase gamma subunit precursor (Chlorate reductase heme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ideonella dechloratans.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                   13.1%; Score 66; DB 1; Length 121; 32.9%; Pred. No. 25; tive 12; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.1%; Score 66; DB 1; Length 239; 40.0%; Pred. No. 47; tive 8; Mismatches 18; Indels
                 11930 MW; AD17BD8C67F5537E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Æ
                                                                                                                                                                                                                                                                                                                                                            239 AA.
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                                                                                                                                                                                                                    52 -----GTLNPLKLLLSSL 64
                                                                                                                                                                                                                                              | ||| |::|
71 LTSAVSGRINPQVNLVDTL 89
                                                                                                26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 40.0
ses 20; Conservative
                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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  121
121
121 AA;
                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=36863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wastewater.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      deonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subunit).
NON TER
SEQUENCE
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                                                          Query Match
                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=NCTC 10268;
MEDINES-27218684; PubMed=5066108; Woodward M., Dale J.W.; Woolford A.J., Hewinson R.G., Woodward M., Dale J.W.; Sequence heterogeneity of an mpb70 gene analogue in Mycobacterium
                                                                                                                                                                                                                                                                                     o.
                                                                                                                                                  InterPro; IPRUUUSze; France...

Pfam; PR00234; tryp_alpha_amyl; 1.

PRINTS; PR00332; LIPIDTRNSFER.

SMART; SM00499; AAI; 1.

EROSITE; PS00597; PLANT LTP; 1.

Lipid-binding; Transport; Signal; Multigene family.

Signal.

CHAIN

26 118 NONSPECIFIC LIPID-TRANSFER PROTEIN |

POTENTIAL.

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78
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IMMINGENIC PROTEIN MPT70 ANALOG.
PAS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 ------ANPLGTLNPLKL--LLSSLGIPVNHLIEGSQKC
                                                                                                                                                                                                                                                                                                                                                                                                                          13.1%; Score 66; DB 1; Length 118; 22.7%; Pred. No. 25; ive 18; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Immunogenic protein MPT70 analog precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
53214BCDC4491DFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kansasii.";
FEMS Microbiol. Lett. 148:43-48(1997).
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SIMILARITY: Contains 1 PASI domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AA
    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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INTERFPO. IPRO00782, B19H3 FAS1.
Pfam; PFO2469; Fasciclin; I.
PROSITE; PSS0213; FAS1; 1.
                                           EMBL; L29767; AAA32995.1; -.
EMBL; L33907; AAA73948.1; -.
PIR; S45680; S45680.
HSSP; P19656; 1MZM.
HRSP; P19656; 1MZM.
InterPro; IPR003612; AAI.
InterPro; IPR00528; Plant_LTP.
                                                                                                                                                                                                                                                                  25 10
26 118 NON
29 77 NON
39 54 POT
55 100 POT
75 114 POT
118 AA, 11937 MW; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
>121
>121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium kansasii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1768;
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55
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Q49614;
                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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SIGNAL
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 27
MP70 MYCKA
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7

Gaps

4,

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MEDLINE=22825698; PubMed=12917642; Malfatti S., Chain P., Ancapa G., Larimer F.W., Lamerdin J., Malfatti S., Chain P., Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M., Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A., Webb E.A., Zinser E.R., Chisholm S.W.; "Genome divergence in two Prochlorococcus ecotypes reflects oceanic niche differentiation.";
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
2-isopropylmalate syxthase (EC 2.3.3.13) (Alpha-isopropylmalate synthase) (Alpha-IPM synthetase).
                                                                Prochlorococcus marinus (strain MIT 9313).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                            NCBI_TaxID=74547;
                                          synthase) (Alpha
LEUA OR PMT1121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                              PEQUENCE FROM N.A., AND SEQUENCE OF 312-341.

MEDLINE=92105132; PubMed=1722210;

A Bothwell A.L.M., Ballard D.W., Philbrick W.M., Lindwall G.,

A Maher S.E., Bridgett M.M., Jamison S.F., Garcia-Blanco M.A.;

Mather S.E., Bridgett M.M., Jamison S.F., Garcia-Blanco M.A.;

Mather Dolypyrimidine tract binding protein. Purification, cloning,

I J. Biol. Chem. 266:24657-2463(1991).

I J. Biol. Chem. 266:24657-2463(1991).

-!- FUNCTION: Plays a role in pre-mRNA splicing. Binds to the
polypyrimidine tract of introns. May promote the binding of U2

snRMPH to pre-mRNA.

-!- SUBUNIT: Part of a ternary complex containing FUBP2, PTBP1, PTBP2

and HNRPH1 (By similarity).

-!- SUBCELLULAR LOCATION: Nuclear.

-!- DOMAIN: The C-terminal 195 amino acids of PTB are sufficient for

specific RNA binding.

-!- SIMILARITY: Contains 4 RNA recognition motif (RRM) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 ALSCSSAAAF-----LVGSAKPVAQPVAALESAAE-----AGAGTLANPLGTLNPLK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 SLDQTMAAAFGLSVPNVHGALAPLAIPSAAAAAASRIAIPGLAGAGNSVLLVSNLNPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 VIPOSLFILFGVYGDVQRVKILFNKKENALVQMADGSQAQLGEPPERAQAAREVSA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 LILSSLGI------PVNHLIEGSQKCVAELG--PQAVGAVKALKA 95
             01-AUG-1990 (Rel. 15, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Polypyrimidine tract-binding protein 1 (PTB) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I).
                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.1%; Score 66; DB 1; Length 527; 26.7%; Pred. No. 94; cive 16; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    540 AA
                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 26.7%
                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412 VQVSCGS-----SLRPTATVILAQEDGQEQTAAAVGT--GPVDAVCRALNALAGEPNE 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70
Nature 424:1042-1047(2003).

-!- FUNCTION: Catalyzes the condensation of the acetyl group of acetyl-CoA with 3-methyl-2-oxobutanoate (2-oxoisovalezate) to form 3-carboxy-3-hydroxy-4-methylpentanoate (2-isopropylmalate).
-!- CATALYTIC ACTIVITY: Acetyl-CoA + 3-methyl-2-oxobutanoate + H(2)0 = 2-hydroxy-2-isopropylsuccinate + CoA.
-!- PATHWAY: Leucine biosynthesis; first step.
-!- SUBUNT: Homorteramer (By similarity).
-!- SUBUNT: Homorteramer (by similarity).
-!- SIMILARITY: Belongs to the alpha-IPM synthetase / homocitrate synthase family. LeuA l subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 VALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthesis; Transferase; Complete proteome.
540 AA; 57970 MW; A68C195F7E8FE7DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
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NUP1 RAT

AC P70581, Q9CHE1, Q9CMK7; Q9Z2W7;

DT 10-0CT-2003 (Rel. 42, Last sequence update)

DT 10-0CT-2003 (Rel. 42, Last sequence update)

DT 10-0CT-2003 (Rel. 42, Last annocation update)

DT 10-0CT-2003 (Rel. 42, Last annocation update)

MUS1-0CT-2003 (Rel. 42, Last annocation update)

GN NUP1-1.

ON NUP1-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, BX572099, CA221296.1; --
HAMAP, MF 01025, -; 1.
InterPro; IPR002034; AIPM/Hoit synth.
InterPro; IPR00891; HAGL-like.
InterPro; IPR008691; LeuA bact_synth.
IGREAMS; TIGR00571; LeuA bact_synth.
IIGRFAMS; TIGR00973; leuA bact; 1.
PROSITE; PS00815; AIPM HOMOCIT_SYNTH 1; 1.
Leucine biosynthesis; Transferase; Complete F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
13.1%; Score 66; DB 1
Best Local Similarity 32.5%; Pred. No. 96;
Matches 26; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIEFSVKSVTE-GIDAMGEV 481
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similarity/.
-!- SIMILARITY: Belongs to the eutC family.
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                                                                                                                                                                                                                                                                                                                                                Missing (Ir/FTId=VSP_(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      585 AA; 59265 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
13.1%
Best Local Similarity 27.5%
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1833;
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TISSUE-MACTOPAGE.

MEDLINE-9013879; PubMed=9795236;

MEDLINE-9013879; PubMed=979526;

MEDLINE-9013879; PubMed=979526;

MEDLINE-9013879; PubMed=97979;

MEDLINE-9013879; PubMed=979529;

MEDLINE-9013879; PubMed=979539;

MEDLINE-9013979; PubMed=979539;

MEDLINE-9013979;
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  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS P45 AND P23), SEQUENCE OF 309-585 FROM N.A. (ISOFORM H6), AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isoid=P70581-2; Sequence=VSP_008579, VSP_008580, VSP_008581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lsoid=P70581-3; Sequence=VSP_008576, VSP_008577, VSP_008578,
VSP_008582;
                                                                                                                                                                                                             MEDLINE=563266665, PubMed=8707840;
Hu T., Guan T., Gerace L.; Molecular and functional characterization of the p62 complex, an assembly of nuclear pore complex glycoproteins.";
J., Cell Biol. 134:589-601(1996).
                                                                             SEQUENCE FROM N.A. (ISOFORM PSB), SEQUENCE OF 227-237; 317-333; 409-422 AND 427-433, ALTERNATIVE SPLICING, FUNCTION, SUBCELLULAR LOCATION, IDENTIFICATION IN A COMPLEX WITH NUP62 AND NUP54, AND INTERCITION WITH NUFF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U63839; AAC52789.1; -.
EMBL; AF000898; AAC62539.1; -.
EMBL; AF000901, AAC62318.1; -.
EMBL; AF000901, AAC62319.1; -.
Transport; Nuclear protein; Repeat; Coiled coil; Glycoprotein; Alternative splicing.
Alternative 57 565 14 X 2 AA REPEATS OF F-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isold=P70581-4; Sequence=VSP_008583, VSP_008584; Note=No experimental confirmation available; TISSUE SPECIFICITY: Expressed in liver. DOMAIN: Contains F-G repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 X 2 AA REPEATS OF F-G
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COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PTM: O-glycosylated.
-!- SIMILARITY: Belongs to the NUPL1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isold=P70581-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COILED (
                                                                                                                                                                                                     TISSUE=Macrophage;
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                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Ethanolamine ammonia-lyase light chain (EC 4.3.1.7) (Ethanolamine ammonia-lyase small subunit).
PADYFRVLVQ -> SPDDERLQVH (in isoform
                                                                                                                                                    /FIGEVER (10 isoform p45).
/FIGEVER (10 isoform p45).
/FIGESS -> LCASA (in isoform p45).
/FIGEVER (10 isoform p45).
/FIGEVER (10 isoform p45).
/FIGEVER (11 isoform p45).
/FIGEVER (11 isoform p23).
/FIGEVER (11 isoform p45).
/FIGEVER (11 isoform p46).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 TPATTTAASTGLSLGGALAGLGGSLFOSGNTATSGLGONALSLSLGTAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 NPLKLLLSSLGIPVNHLIEGSQKCVAELGPQAVGAV--KALKALLGALT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Nocardiaceae, Rhodococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.1%; Score 66; DB 1; Length 585; 27.5%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48; Indels
                                          /FTId=VSP 008576.

70P -> DGW (in isoform p23)

/FTId=VSP 008577.

14ssing (in isoform p23).

/FTId=VSP_008578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                4D5F5C2744A75C3C CRC64;
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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
web by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   130 SALVTALGERYSIAPPVIATNARVALGDHIAAAMGVQTAIVLIGE-RPGLSVADSVGIYL 188
                                                                                                                                                                                                                                                                                                                                            17 SAAAFLVGSAKPVAQPVAALES-----AAEAGAGTLANPLGTLNFLKLLLSSLGIPV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
110-0CT-2013 (Rel. 42, Last annotation update)
110-0CT-2013 (Rel. 42, Last annotation update)
110-0CT-2013 (NN:DBI PRT) (N(1)-alpha-phosphoribosyltransferase)
110-0CT-2013 (NN:DBI PRT) (N(1)-alpha-phosphoribosyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MAPF303099;
MEDLINE=21082930; PubMed=11214968;
Raneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Res. 7:331-38(2000).

Res. 7:331-38(2000).

FUNCTION: Catalyzes the synthesis of alpha-ribazole-5'-phosphate from nicorite monoucleotide (NAMN) and 5,6-dimethylberaimidazole (DMB).

CATALYZIC ACTIVITY: Beta-nicotinate D-ribonucleotide + dimethylbenzimidazole - nicotinate + N(1)-(5-phospho-alpha-D-ribosyl)-5,6-dimethylbenzimidazole.

PATHWAY: Cobalamin biosynthesis.
                                                                                                                                                                                                                                                           Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                              257 AA; 26963 MW; E6E3FA138F49C91B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    41;
                                                                                                                                                                                                                                                                                                                                                                                                                             69 NHL----IEGSQKCVAEL-GPQAVGAVKALKALLGALT
                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                       13.0%; Score 65.5; Di
25.3%; Pred. No. 55;
live 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF 00230; -; 1.
InterPro; IPR003200; NN:DBI PRT.
InterPro; IPR008281; NN:DBI PRT sub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP002997; BAB48775.1; -.
                                                                                                                                                  EMBL; 124492; AAC37137.1; -.
HAMAP; MF_00601; -; 1.
                                                                                                                                                                                                                                                                                                    25; Conservative
                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=381;
                                                                                                                                                                      HAMAP; MF 00601
Lyase; Cobalt.
SEQUENCE 257
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                   224 ALGGRELAAIFGATLAARHIGIPV--LLDGF-VCTAAAAPLARLHPTGLSHTIAAHVSAE 280
                                                                                                                                                                                                                                            7 IGLCVALSCSSAAAFLVGSAK------PVAQPVAALESAAEAGAGTLANPLGTLN 55
                                                                                                                                                                                                                                                                                                                                        56 PL------KLLLSSLGIPVNHLIEGSQKCVAELGPQA-------VGAV 90
                                                                                                                                                                                                                                                                                          164 IGNTTPAAAISAALFGGGAEKWTGRGTGVDDAGLKRKVVAIEAGLKRHAAALADPLGVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nalson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Blishai W., Jacobs W.R. Lr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=9829587; PubMed=9634230;
Cole S.T., Brogch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brogch R., Parkhill J., Garnier T., Churcher C., Harris Coledordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Erown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeper K., Skelton S., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Complete genome sequence esquence squares Nature 393:537-544 (1998).
                                                                                                                                                                                                   39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
Pfam; PF02277; DBI_PRT; 1.
ProDom; PD009438; NN:DBI_PRT; 1.
Cobalamin biosynthesis; Porphyrin biosynthesis; Transferase; Glycosyltransferase; Complete protecome
ACT_SITE 304 304 BASE (BY SIMILARITY)
SEQUENCE 336 AA; 34408 MW; F9824D6693745932 CRC64;
                                                                                                                                                          DB 1; Length 336;
                                                                                                                                                     s; Score 65.5; DB 1; Length 3
s; Pred. No. 70;
12; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laboratory strains ";
J. Bacteriol. 184:5479-5490(2002).
- SIMILARITY: Belongs to the UPF0089 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
110-CCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein Rv2484c/MT2557.
Wycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491 AA
                                                                                                                                                          13.0%;
26.9%;
                                                                                                                                                                             Local Similarity 26.9%
Les 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                   91 KALKALLGAL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 SGHRRLLEAL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1773;
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                                                                                                                                                       Query Match
Best Local S
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Pred. No.

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Best Local Similarity 27.6
Matches 27; Conservative
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Matches
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YM96_SYNEL
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                                                                                                                                                                                                                        4 AALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAG-----TLANPLGTLNPL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: Anthranilate + phosphoribosyldiphosphate = No. -phosphoribosyl-anthranilate + diphosphate.
PATHWAY: Tryptophan biosynthesis; second step.
SIMILARIY: Belongs to the anthranilate phosphoribosyltransferase
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tryptophan biosynthesis; Transferase; Glycosyltransferase; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnanc S., Demange N., Gaspin C., Lavine M., Moisan A., Robert C., Saurin W., Schiex T., Weissenbach J., Boucher C., Saurin W., Schiex T., Weissenbach J., Boucher C.A., Michael Sequence of the plant pathogen Ralstonia solanacearum.", Nature 415:497-502(2002)
                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid megaplasmid.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                    DB 1; Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 344;
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Anthranilate phosphoribosyltransferase 2 (EC 2.4.2.18).
TRPD2 OR RSP0681 OR RS01768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65074865254E2FF2 CRC64;
               EMBL; AL021246; CAA16061.1; -.
EMBL; AE007092; AAK46861.1; -.
PIR; C70868; C70868.
TIGR; MI2557; -.
Tuberculist; Rv2484c; -.
InterFro; IPR004255; UPF0089.
Pfam; PF03007; UPF0089.
Pfam; PF03007; UPF0089.
FYPOCHERICAL protein; Complete protecme.
SEQUENCE 491 AA; 52309 MW; C2ACCE458ADF82DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                                                                23;
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                                                                                                                                                                              8; Mismatches
                                                                                                                                                    Score 65.5; I
Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MF_00211; -; 1.
InterPro; IPR005940; Ant_phepho_trans.
InterPro; IPR00312; Glyco_trans_3.
Pfam; PF00591; Glyco_trans_3N; 1.
Pfam; PF00591; Glyco_trans_3N; 1.
Pr000m; PD001864; Glyco_trans_3; 1.
IIGRFAMS; TIGR01245; trpD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL646080; CAD17832.1; -.
HAMAP; MF_00211; -; 1.
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                                                                                                                                                      13.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Burkholderiaceae; Ralstonia.
                                                                                                                                                       Query Match
Best Local Similarity 36.7
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=305;
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Q8XS00;
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Score 65;

12.9%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 ALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIJNE=22225144; PubMed=12240834;
Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
Nakanaba A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
Katanaba A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N.,
Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the thermophilic cyanobacterium
Thermosynechococcus elongatus BP-1.";
DNA Res. 9:123-130(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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                               29; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synechococcus elongatus (Thermosynechococcus elongatus
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 IEGSOKCVAEL-----GPOAVG-AVKALKALLGALTVF 103
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                                                                                                                                                                                        75 SQKCVAELG-----PQAVGAVKALKAL---LGALTVF 103
                                                                                                                                                                                                                             AZAC HUMAN STANDARD; FRT; 462 AA. P18825; P35369; Q9HB49; O1-NOV-1990 (Rel. 16, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0272 protein t112296.
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  ed. No. 79;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   399
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27.6%; Pre-
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399 AA; 43522 MW;
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Interpro; IPR002822; DUF111.
Pfam; PF01969; DUF111; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOLSES; DUFILL; 1.
PD018127; DUF111; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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Best Local Similarity
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SEQUENCE 39
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STRAIN=K12
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Best Local &
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SOTAL STATE TO THE STATE TO THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).

Yano K., Takeda M., Sugimoto E., Sagai H.;

"Molecular Cloning and expression of a novel human alpha2C-adrenerginc
"receptor, alpha2CII, gene.";

Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                         MEDLINE=88320430; PubMed=2842764;
Regan J.W., Kobilka T.S., Yang-Feng T.L., Caron M.G., Lefkowitz R.J.,
Kobilka B.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   catecholamine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isold=P18825-2; Sequence=VSP_001863;
POLYMORPHISM: The Deli32-325 variant has a significant loss of
function. It is approximately 10 times more frequent in African-
Americans compared with Caucasians (allele frequencies 0.381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20390061; PubMed=10801795;

MEDLINE=20390061; PubMed=10801795;

Small K.M., Forbes S.L., Rahman F.P., Bridges K.M., Liggett S.B.;

"A four amino acid deletion polymorphism in the third intracellular loop of the human alpha 2C-adrenergic receptor confers impaired coupling to multiple effectors:";

J. Biol. Chem. 275:23059-23064(2000).

-i. FUNCTION: Alpha-2 adrenergic receptors mediate the catecholamine induced inhibition of adenylate cyclase through the action of G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               versus 0.040).
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                               the promoter
                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
Alpha-2C-adrenergic receptor (Alpha-2C adrenoceptor) (Subtype C4)
ADRA2C.
                                                                                                                                                                                                                                                        "Cloning and expression of a human kidney cDNA for an alpha 2-adrenergic receptor subtype.";
Proc. Natl. Acad. Sci. U.S.A. 85:6301-6305(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 104220; -.
GO:000576B; C:endosome; TAS.
GO:0005887; C:integral to plasma membrane; TAS.
GO:0004938; F:alpha2-adrenergic receptor activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98041882; PubMed-9371698; Schaak S., Devedjian J.C., Cayla C., Sender Y., Paris H.; Wolecular cloning, sequencing and functional study of the region of the human alpha2C4-adrenergic receptor gene."; Biochem. J. 328:431-438(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins.
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P18825-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 2).
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EMBL, U72648; AAC78723.1; -.
EMBL, D13538; BAAC2737.1; -.
EMBL, AF280399; AAG28076.1; -.
EMBL, AF280400; AAG28077.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AF280400, AAGZ8077.
PIR, A31237; A31237
HSSP, P29274; IMMH.
Genew, HGNC:283; ADRAZC.
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                                    ., TAS
                                                                                           PRINTS, PRO0217, GPCRRHODOPSN.

PROSITE, PS00237, G-ROTEIN_RECEP_F1_1; 1.

PROSITE; PS00237, G-ROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor, Transmembrane, Glycoprotein;

Multigene family; Phosphorylation; Polymorphism; Alternative splicing.

DOMAIN

51

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 AAAFLVGSAKPVAOPVAALESAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNHLIEGSQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 AAALAVAAA---AGPNAS--GAGERGSGGVANASG-----ASWGPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92041567; PubMed=1938888;
Lloyd R.G., Sharples G.J.;
"Molecular organization and nucleotide sequence of the recG locus of
Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGENGHCAPPPADVEPDESSAAAERRRRGA -> EART
ARPRPPTWSRTRAAQRPRGGAPGP (in isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia. NCBI_TaxID=562;
GO: GO:0000187; P:activation of MAPK; TAS.
GO: GO:0007267; P:cell-cell signaling; TAS.
GO: GO:0007186; P:G-protein coupled receptor protein signalin. .
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PP00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
ARGALICH (BASIC).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 65; DB 1; Length 462;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L -> R (IN REF. 1 AND 2).
E -> Q (IN REF. 1 AND 2).
S -> I (IN REF. 1 AND 2).
S -> I (IN REF. 1 AND 2).
R -> P (IN REF. 1 AND 2).
4; E1EF9CA21E7F6EDA CRC64;
                                                                                                                                                                                                                                                                                                                                                               5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                          4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VAR 012747.
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TREGG ECOLI

STANDARD;

PRT; 693 AA.

( P24250; P76721;

DT 01-WAR-1992 (Rel. 21, Created)

DT 01-WAR-1992 (Rel. 21, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE ATP-dependent DNA helicase recG (EC 3.6.1.-).

GN ESCG OR B3652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49522 MW;
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32.6%;
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329
401
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446
462 AA;
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77
77
89
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1115
1125
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                                               298 VGSGKTLVAALAALRAIAHGKQVALMAPTELLAEQHANNFRNWFAPLGIEVGWL-AGKQK 356
23 VGSAKPVAQPVAALESAAEAGAGTLANPLGTL----NPLKLLLSSLGIPVNHLIEGSQK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                undiminate and cent addression invectores at the indeed of account initial segments.

-!- SUBUNIT: Neural-specific isoforms may be a constituent of a neurofascin/NRCAM/ankyrin G complex.

-!- ALTERNATIVE PRODUCTS:

-- EVERTATIVE PRODUCTS:

-- EVERTATIVE SPORTING SPORTING isoforms are produced;

Name-1; Synonymes of isoforms are produced;

Name-1; Synonymes of isoforms are produced;

-- ISSUE SPECIFICITY: Expressed in brain and other tissues. Isoform 1 is neural-specific.

-- ISSUE SPECIFICITY: ANY repeats.

-- SIMILARITY: Contains 1 death domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB-Brain stem;
MEDIATE-97138209; PubMed-7836469;
MEDIATE-97138209; PubMed-7836469;
MEDIATE-97138209; Debmedt V.;
"Ankyring. A new ankyrin gene with neural-specific isoforms localized at the axonal initial segment and node of Ranvier."
The axonal initial segment and node of Ranvier."
J. Biol. Chem. 270:2352-2359(1995).
I- FUNCTION: Membrane-cytoskeleton linker. The neural-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoforms may participate in the maintenance/targeting of ion channels and cell adhesion molecules at the nodes of Ranvier and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                 28-FBB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ankyrin 3 (ANK-3) (Ankyrin G).
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GO; GO:0006605; P:protein targeting; NAS.
                                                                                                         78 CVAELGPOAVGAVKALKALLGALTVF 103
                                                                                                                                      357 GKARLAQQEAIASGQVQMIVGTHAIF 382
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PS50297, ANK REP REGION; 1.
PS50017; DEATH DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
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InterPro; IPR002110; ANK.
InterPro; IPR000488; Death.
InterPro; IPR000488; Death.
Pfam; PF00023; ank; 24.
Pfam; PF00753; Genth; 1.
PF1am; PF00791; ZU5; 1.
PRINTS; PR01415; ANKYRIN.
SWART; SW000548; ANK; 21.
SWART; SW000548; ZU5; 1.
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                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC: 494; ANK3.
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HSSP; P55273; 1B18.
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PROSITE; E
PROSITE;
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012955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95292979; PubMed=1774596;
Hong X., Cadwell G.W., Kogoma T.;
"Escherichiad coli RecG and RecA proteins in R-loop formation.";
"Escherichiad coli RecG and RecA proteins in R-loop formation.";

EMBO J. 14:2385-2392(1995).

-!- FUNCTION: Critical role in recombination and DNA repair. Help
process Holliday junction intermediates to mature products by
catalyzing branch migration intermediates to mature products by
catalyzing branch migration intermediates to mature products by
catalyzing branch migration. Has a DNA unwinding activity recG
unwind branched duplex DNA (Y-DNA). Has a role in constitutive
stable DNA replication (csdR) and R-loop formation.

-!- SIMILARITY: Belongs to the helicase family. RecG subfamily.
                                                                                                                                                                                                                                                          SEGUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=93315143; PubMed=7686882;
MEDLINE=93315143; PubMett G. III, Daniels D.L., Blattner F.R.;
"DA sequence and analysis of 136 kilobases of the Escherichia coli genome: organizational symmetry around the origin of replication.";
Genomics 16:551-561(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGREAMS; TIGRO0643; recg; 1.
Hydrolase, Helicase; DNA repair; ATP-binding; DNA recombination; DNA-binding; Complete proteome.
NP_BIND 296 303 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95045415; PubMed=7957087;
Mhitby M.C., Vincent S.D., Lloyd R.G.;
"Branch migration of Holliday junctions: identification of RecG
protein as a junction specific DNA helicase.";
EMBO J. 13:5220-5228(1994).
                                                                                                                   MEDLINE=92184121; PubMed=1544582; Kalman M., Murphy H., Cashal M.; Murphy H., Cashal M.; The mucleotide sequence of recG, the distal spo operon gene in Escherichia coli K-12."; Gene 110:95-99(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEQH BOX. 7826143A8F4292A2 CRC64;
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EMBL; M64367; AAA24513.1; ---
EMBL; L10328; AAA6205.1; ---
EMBL; AE000442; AAC76676.1; ---
EMBL; AH0265; JH0265.
ECOGENE; EG10829; xecG.
INTERPRO; IPR001410; DEAD.
INTERPRO; IPR0014010; DEAD.
INTERPRO; IPR008994; Nucleic_acid_OB.
INTERPRO; IPR008994; Nucleic_acid_OB.
INTERPRO; IPR0084365; tRNA_anti.
Pfam; PF00270; DEAD; 1.
Pfam; PF00270; DEAD; 1.
SMART; SM004807; DEAD; 1.
SMART; SM004807; DEAD(1.
                  Bacteriol. 173:6837-6843(1991)
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693 AA; 76430 MW;
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Best Local Similarity 30.2
Matches 26; Conservative
                          J. Bacteriol. 173:
[2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION
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-!- FUNCTION: MAY BE INVOLVED IN ELECTRON TRANSFER FROM B-C1 COMPLEX
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BINDING
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1665 TSAAPLISSPLKSSVVSPVKSRVDVISSAKITMASSLSSPVKQMPGHAEVALVNGSISPLK 1724
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MEDLINE=92041558; PubMed=1657867;
Bott M., Ritz D., Hennecke H.;
"The Bradyrhizolum japonicum cycM gene encodes a membrane-anchored homelog of mitochondrial cytochrome c.";
J. Bacteriol. 173:6766-6772(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-USDA 110;
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Saesmoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110."; bNA Res. 9:189-197(2002).
                                                                            113 158 ANK 4.
203 230 ANK 5.
234 253 ANK 6.
235 ANK 6.
236 ANK 7.
330 329 ANK 7.
336 395 ANK 10.
339 428 ANK 11.
452 494 ANK 11.
458 527 ANK 13.
458 527 ANK 13.
550 ANK 13.
551 550 ANK 14.
551 550 ANK 15.
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556 ANK 20.
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559 693 693 ANK 20.
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Bradyrhizobiaceae, Bradyrhizobium.
NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1725 YASSST-----LINGC-KATATLQEKISSATNSVSSVVSAAT 1760
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splicing; Repeat; ANK repeat.
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01-APR-1993 (Rel. 25, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
CYCOLDONG C homolog.
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Best Local Similarity 26.2%
Matches 27, Conservative
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Cytoskeleton;
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CYCM BRAJA
ID CYCM BRAJA
AC P30323;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (POTENTIAL).
PERIPLASMIC (POTENTIAL).
HEME (COVALENT) (BY SIMILARITY).
HEME (COVALENT) (BY SIMILARITY).
IRON (HEME AXIAL LIGAND) (BY SIMILARITY)
IRON (HEME AXIAL LIGAND) (BY SIMILARITY)
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Best Local Similarity 26.9%; Pred. No. 50;
Matches 28; Conservative 14; Mismatches 39; Indels 23; Gaps
                                                                                                                                                                                                                                                                                    10 CYTOPLASMIC (POTENTIAL).
31 SIGNAL-ANCHOR (POTENTIAL).
184 PERIPLASMIC (POTENTIAL).
84 HEME (COVALENT) (BY SIMILARI'
87 HEME (COVALENT) (BY SIMILARI'
88 IRON (HEME AXIAL LIGAND) (BY
151 IRON (HEME AXIAL LIGAND) (BY
151 KON (HEME AXIAL LIGAND) (BY
19098 MW; ZECDCFA564389824 CRC64;
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TO AA3.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
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Q821n6 streptomyce
Q8fs1 corynabace
Q9k3q4 streptomyce
Q9scr1 rhizobium 1
Q9su8 arabidopsis
Q8xx23 rarebidopsis
Q7xy5 brdetella
Q7vya1 bordetella
Q7vya1 bordetella
Q7vya1 bordetella
Q86691 streptomyce
Q8th10 methanosarc
Q8uai4 agrobacteri
Q9abl caulobacteri
Q94x4 bifidobacter
                                                               April 5, 2004, 14:28:38; Search time 39 Seconds (without alignments) 841.382 Million cell updates/sec
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502
1 MKLAALLGLCVALSCSSAAA......QAVGAVKALKALLGALTVFG
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                protein search, using sw model
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106 LAGFLGLCIGNLRAGAPMADAMDHALAHTTGSTGSAGPTTVALTAAARRVRSGGSGAAVL 165
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Redd H., Ishtkawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
Sakaki Y., Hattori M., Omura S.;
Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial
red microcapanism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(203).
BMBL; AP005029; BAC69685.1;
RMSL; AP005029; Enethinnyl aminopeptidase activity; IEA.
O; Go:0006209; F:methinnyl aminopeptidase activity; IEA.
RO; Go:0006509; Peptidase M24.
InterPro; IPR001714; Pept M24. MAP.
RINTS; PR00557; Peptidase M24.
InterPro; IPR001714; Pept M24. MAP.
RINTS; RR0059; MAPEPTIDASE.
ITGRRAMS; TIGR00500; met Ddase_I; 1.
Mainopeptidase; Complete proceome.
Mainopeptidase; Complete proceome.
SEQUENCE 255 AA; 26727 MW; OC41CD3010F855A3 CRC64;
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SEQUENCE FROM N.A.
STATAILS 73.14 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
Ibuda Y., Sugimoto S.,
"The entire genomic sequence of Corynebacterium efficiens YS-314.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
BYBL, ABOOS215, BAC17109.1, .
Hypothetical protein.
ByBL, ABOOS215, BAC17109.1, .
Hypothetical protein.
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                Horikawa H., Nakazawa H., Osonoe T.
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T. Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium efficiens.
Bacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 17.5%; Score 88; DB 16; Length 255; Local Similarity 31.6%; Pred. No. 2.7; neg 31; Conservative 16; Mismatches 19; Indels
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE-25608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
11-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Conserved hypothetical protein.
CE0299.
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                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
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Q8FST3
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                                                                                    0892W6 ralstonia 8 070114 mycobacteri 005907 mycobacteri 095D37 streptomyce 08znl3 salmonella 08the corynebacte 098m48 rhizobium 1 0898q7 bradythizob
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DECLINE_27326074; PubMed=12438750; Milmi T., Copeland N.G., Gilbert D.J., Jenkins N.A., Srisodsai A., Niimi T., Copeland N.G., Gilbert D.J., Jenkins N.A., Srisodsai A., Zimonjic D.B., Keck-Waggoner C.L., Popescu N.C., Kimura S., Cloning, expression, and chromosomal localization of the mouse gene (Scgb31a, alias Ugrp2) that encodes a member of the novel uteroglobin-related protein gene family "; Cytogenet. Genome Res. 97:120-127(2002).

EMBL, ARS13467, ARM62328.1; --
MGD, MGI:1915912; Scgb3a1. 7C84B908A6365B59 CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces avermitilis.
Bacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
Straptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.8%; Score 225; DB 11; Length 94; 57.3%; Pred. No. 2e-13; cive 14; Mismatches 20; Indels
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TRAIN-MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE-21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative methionine aminopeptidase.
SAV1974.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                           QBY2W6
Q7U114
Q7U114
Q9FB37
Q8ZNL3
Q8ZNS
Q8ZS99
Q8NT86
Q98M486
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01-MAR-2003 (TrEMBLrel. 23, C;
01-MAR-2003 (TrEMBLrel. 23, L;
01-MJV-2003 (TrEMBLrel. 24, L;
UGRP2 type B.
SCGB3A1.
                                                                                                  51; Conservative
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PIR, T09931, T09931.

GO, GO:0016787, F:hydrolase activity; IEA.

GO, GO:0004551, F:hydrolase activity; IEA.

GO, GO:0009117, P:nucleotide diphosphatase activity; IEA.

InterPro; IPR002591, Phosphodiest.

Pfam; PF01663; Phosphodiest; 1.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO/9344; CAB45328-1; --
EMBL; ALO(555; CAB79726-1; --
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Q9SU83
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                          166 IDAPTMDLQRLGTIWEVSERHGIPLVRLLDQL----KHRLEAQERHRQASAAQLQGPQAT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NALAALAGAVNPATALAGVTNPLAALGGIGAAGNPLAGLAAGAAGPLGNIAGAAQNPLAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 SAAAFLVGSAKP-----VAOPVAALESAAEAG-----AGTLANPLGTL-----NPLKL 59
48 ANP-----LGTL-----NPLKLLLSSLGIPVNHLIEGS----OKCVAEL-GPQAV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                   MEDLINE-21996410; PubMed=12000953; MEDLINE-21996410; PubMed=12000953; MEDLINE-21996410; PubMed=12000953; MEDLINE-21996410; PubMed F. R. Cardeno-Tarraga A.-M., Kieser H., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harris D.E., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K. Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; A199108; CAB99157.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 247 AA; 22950 MW; EB32ABD76146881B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.4%; Score 82.5; DB 16; Length 247; 31.8%; Pred. No. 8.3; tive 10; Mismatches 40; Indels 23.
                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 LTGAAGGGNPLAAALGGAGNPLAALG----GAANPLAAVGGAAGALG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                            01-0cr-2000 (TrEMBLrel. 15, Created)
01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SC01277.
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01-007-2001 (TrEMBLrel. 18, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein mlr5043.
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MEDLINE=21082930; PubMed=11214968;
                                                     88 GAVKALKALLGAL 100
                                                                                222 AVILALIPLAGVL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                        Streptomyces coelicolor.
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Q98CR1
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438 MVPLFGISEAMDAAGAAAFIGWAWAEPOAOPVDT-~SAAGAAGG-----GHVTPDEAEA 489
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Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Tabata S., Takeuchi C., Yamada M., Tabata S.; Mirogen-fixing symbiotic bacterium Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LAALLGLCVALSCSSAAAFLVGS-AKPVAQPVAALESAAEAGAGTLANPLGTINP----L
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01-MAY.2000 (TEMBLEEL. 13, Last sequence update)
01-OCT-2003 (TEMBLEEL. 25, Last annotation update)
01-OCT-2003 (TEMBLEEL. 25, Last annotation update)
116L4.190 OR AT4G29680.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Etreptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16; Length 694;
                                                                                                                                                                                                                                   REMEL, AD003005; BAE515601, ...
RMEL, AD003005; BAE515601, ...
GO, GO:0005524; F:Catalytic activity; IEA.
GO; GO:0005524; F:Catalytic activity; IEA.
GO; GO:000512; F:CRNA ligase activity; IEA.
GO; GO:0006418; P:metabolism; IEA.
GO; GO:0006418; P:metabolism; IEA.
GO; GO:000812; P:metabolism; IEA.
RILEFPEO; IPRO03811; Coalbinding.
RILEFPEO; IPRO03811; Coalbinding.
RILEFPEO; IPRO1412; ENRA-synt I.
R PFAm; PFO2629; Coalbinding; 1.
R PFAm; PFO2629; Coalbinding; 1.
R PROSITE; ES00178; AA_TRNA-LIGASE_I; 1.
R HYPOCHECICAL POTOCHER; Complete protecome.
SEQUENCE 694 AA; 73126 MW; 1954978531DCF6CC CRC64;
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16.4%; Score 82.5; DB 16; Length
Best Local Similarity 33.3%; Pred. No. 25;
Matches 33; Conservative 11; Mismatches 42; Indels
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databases.
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ROBE M., Hempel S., Entian K.-D., Mewes H.W.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
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4 AALLGLCVALSCSSAAAF----LVGSAKPVAQPVAA------LESAAEAGA 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
NAt. Biotechnol. 21:526-531(2003).
EMBL; AP005022; BAC68003.1; -.
Complete proteome.
SEQUENCE 136 AA; 13687 MW; 8273376F70E3EBE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba
Sakaki Y., Hattori M., Omura S.;
                                        MEDLINE=21477403, PubMed=11572948;
MEDLINE=21477403, PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.7%; Score 79; DB 16; Length 136; 33.9%; Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
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Pred. No. 22;
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EMBL; BX640445; CAE33127.1; -.
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STRAIN=RB50 / ATCC BAA-588;
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Matches 40; Conservative
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Best Local Similarity
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Q7WJ66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 LARALGLCELLARCKSVPA--IDPGKPPAMDPASGNATPPASVSAAQNLGDIIVG-LRAPT 75
                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                        6 LLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGA--GTLANPLGTLN-PLKLLLS
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"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502 (2002).
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomycee.
NCBI TaxID=33903;
                                                                           DB 10; Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.9%; Score 80; DB 16; Length 148; 31.1%; Pred. No. 8.1; ive 13; Mismatches 43; Indels
                                                                                                                                             14; Mismatches 17; Indels
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                            54678 MW; 8DC2B4346121D732 CRC64;
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Last annotation update)
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Last annotation update)
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EMBL, AL646071, CAD16359.1, -.
InterPro. IPRO00437, Prok lipoprot S.
PROSITE; PSO0013; PROKAR LIPOPROTEIN; 1.
                                                                        16.1%; Score 81;
Local Similarity 41.3%; Pred. No.
les 26; Conservative 14; Mismarr
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MEDLINE=21681879; PubMed=11823852;
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25, Probable lipoprotein. RSC2652 OR RS04564.
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                                        496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     114 SDG 116
                                                                                                                                                                                                                                                                                                                                63 SLG 65
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            Hydrolase.
                                                                                           Query Match
Best Local S:
Matches 26;
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                                        SECUENCE
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Indels

43;

Q8XW23 RESULT 7 Q8XW23

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STRAINERSON ALCUE MANDESSIGNATION BY ALCUE MANDESSIGNATION BY ALCUE MANDESSIGNATION BY ALCUE MANDESSIGNATION BY SEASING MANDESSIGNATION BY ACTUAL BY ALTHOUGH BY AMORE MANDESSIGNATION BY ACTUAL BY AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=518;
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
BB2634.
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RESULT 8

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                    Query Match
Best Local
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STRAIN=12822 / ATCC BRA-587;

MATMI=12822 / ATCC BRA-587;

MATMINIT J., Sebaihia M., Pereston A., Murphy L.D., Thomson N.,

A achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach T.,

A chtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach T.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Pethwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Mathy S., Simmond M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitchead S., Barrell B.G., Maskell D.J.,

"Comparative analysis of the genome sequences of Bordetella pertussis,

Bordetella parapatussis and Bordetella bronchiseptica.";

Mathy Box S., Salsa-40(2003).

BMBL, BX640427; CAB36858.1; -.

Complete proteome

200 128.
                                                   144 VQAALASAASFAVGAALPLAIAMAA-------PIAQLMPVVIAGSVAGLGILG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 VALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNH 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 VALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNH 70
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 23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                  Bordetella parapertussis.
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Alcaligeneceae, Bordetella.
NCB. TaxID=519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.4%; Score 77.5; DB 16; Length 229; 32.0%; Pred. No. 22; ive 15; Mismatches 30; Indels 23
 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 AA; 22750 MW; 5A04498C4875195F CRC64;
                                                                              71 LIEGSQKCVAELGPQAV-----GAVKALKALLGALTVFG 104
                                                                                                      190 AV-AARAGGAPVGPAAVRVVLLGAAAMALTAGVGAL--FG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 LIEGSOKCVAELGPOAV-----GAVKALKALLGALTVFG 104
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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 15; Mismatches
                                                                                                                                                                                                   Created)
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BP1449.
Bordetella pertussis.
                                                                                                                                                                                                                                          Putative membrane protein.
 32; Conservative
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                                                                                                                                                                       PRELIMINARY;
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Best Local S
Matches 32
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Q7VYA1;
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Q7WA34
  Matches
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RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13231;

RADLINE=22827954; PubMed=12910271;

RADLINE=22827954; PubMed=12910271;

RA PATKILI U., Sebahia M., Peston A., Murphy L.D., Thomson N., Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L., Achiman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., RA Chillingworth T., Collins M., Cronin A.D., Davis P., Doggett J., Reltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., A leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., RA Babinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K., Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Unvin L., Whitehead S., Barrell B.G., Maskell D.J.;

Tomparative analysis of the genome sequences of Bordetella pertussis, RT Bordetella parapertussis and Bordetella bronchiseptica.";

RT Genet. 35:32-40(2003)

REMBL; BK40415; CAB41739.1; -.

KW Complete proteome.

SEQUENCE 229 AA; 22776 WW; SAIEF22D43DFAZFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 VALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNH 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A3(2) / M145, M146, M14
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Mature 417:1141-147(2002).

EMBL; A19391918; CAA20556.1; -.

PIR; T35084; T35084.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016010; P:transporter activity; IEA.

Interpro; IPR000515; PPD transp.

Pfam; PF00528; PPD transp.

Onnilete professes.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UNY-2093 (TrEMBLrel. 08, Last annotation update)
Putative transport system permease protein.
Putative transport system permease protein.
Streptomyces coelicolor.
Bacteria, Actinobacteria, Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 77.5; DB 16;
; Pred. No. 22;
15; Mismatches 30;
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Pred. No. 63;
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32.0%;
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Matches

8 В ò RESULT 13

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PRT;
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SEQUENCE 355 AA;
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Q9ABL0
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE A ATCC 35395 / DSM 2834;

MEDINE=21929760; PubMed=11932238;

Malchard J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

Allan N., Naylor J., Sange-Thomann N., DeArellano K., Johnson R.,

Linton L., Mardor P., McKernan K., Talamas J., Tirrell A., Ye W.,

Allan N., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

Rerry J.G., Jarrell K.R., Swanson R.V., Zinder S.H., Lander E.,

Metcalf W.W., Birren B.;

The genome of Methanosaccina acetivorans reveals extensive metabolic

and physiological diversity.";

Genome Res. 12:532-542(2002).

REBL, AEGILTO; AAMO7844.1;

Con GO:0004590; Frorotidine-5'-phosphate decarboxylase activity; IEA.

GO; GO:0004590; Frorotidine-5'-phosphate base biosynthesis; IEA.

InterPro; IRR005493; Methyltransf_6.

Refin; PP00125; Owdecase.

Refin; Refinite PP00125; Owdecase.

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                                                                            45
                                                                                                                                                                                                                          46 ------TLANPLGTLNPLKILLSSLGI------PVNHLIEGSQKCVAELGPQ 85
                                                                        3 LAALLGLCVALSCSSAAAFLVGSA--KPVA-----QPVAALESAAEAGAG-----
                                                                                                                                                     126 LVALLVTAVAGSGAATPALAVGAVAWAPLAAHTSSLLRQERATLHITATKGLGAGPVHLL
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        Gaps
        37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea, Buryarchaeota, Euryarchaeota orders incertae sedis,
Methanosarcinales, Methanosarcinaceae, Methanosarcina.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.3%; Score 77; DB 17; Length 453; 27.8%; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Mismatches 34; Indels
        48; Indels
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SEQUENCE 453 AA; 48593 MW; 4863027BB4AEA65D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-UUN-2002 (TrEMBLrel. 21, Created)
1-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein MA4504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ź
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        10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                       86 AVGAVKALKALLGALTV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                        546 AVLAPAAVLALLGALAV 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MĀ4504.
Methanosarcina acetivorans.
            42; Conservative
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Best Local Similarity
Matches 30; Conserv
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QBUAI4
ID QBUAI4
AC QBUAI4;
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62 SSLGIPVNHL-----IEGSQKCVA-----ELGPQAVGAVKALKALLGALTVF 103
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Goodner B., Hinkle G., Gartung S., Miller N., Blanchard M., Mullin L.,
Goodner B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Gelo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent
Science 294:2323-2328(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE-21608550; PubMed=11743193; Monks D.E., Kitajima J.F., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.F., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Roy. P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Samphimachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter, membrane spanning protein.
ATU3389 OR AGE. 2865.
Agrobacterium tumefaciens (strain CS8 / ATCC 33970),
ARIZOBacterium proteobacteria; Alphaproteobacteria; Rhizobium/Agrobacterium group; Agrobacterium.
RNizobium/Agrobacterium group; Agrobacterium.
WCBI_TaxID=176299;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Thio.disulfide interchange protein, putative.
CC0217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G0; G0:0016020; C:membrane; IEA.
G0; G0:0005215; F:transporter activity; IEA.
G0; G0:0006810; P:transport; IEA.
InterPro; IPR000522; FecD.
Pfam; PF01032; FecCD; 1.
ProDom; PD001557; FecCD; 1.
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Pfam; PF00004; AAA; 2.
Pfam; PF02861; Clp N; 2.
PRINTS; PR00300; CLPPROTEASEA.
SWART; SM0382; AAA; 2.
PROSITE; PS00870; CLPAB.1; 1.
PROSITE; PS00871; CLPAB.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Q9F2L6
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SEQUENCE FROM N.A.

SEQUENCE TO 19089 / CB15;

MIDLINE-21176698; PubMed=11259647;

MIDLINE-21176698; PubMed=11259647;

A Midline T. Weldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

A Hoeboy W.T., Durkin A.S., Sephens C., Phadke N.D., Ely B.,

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

A Complete genome sequence of Caulobacter crescenus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

R PMBL, AB025566; ApK22204.1;

TIGR; CC0217;

CO, GO:0015020; C:membrane; IEA.

GO; GO:0017004; P:electron transporter activity; IEA.

GO; GO:0017004; P:electron transporter activity; IEA.

GO; GO:0017004; P:electron transporter activity; IEA.

R InterPro; IPR005663; Thioredox_dom2.

R Press Press
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKL-LL 61
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Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).

EMBL; AE014751; AAN25051.1;

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000166; F:nuclectide binding; IEA.

InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR001270; Chaprin_clpA/B.
InterPro; IPR001270; Chaprin_clpA/B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
   Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
NCBI_TaxID=155892;
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Bacteria, Actinobacteridae, Bifidobacteriales, Bifidobacteriaceae, Bifidobacteriaceae, Bifidobacterium.
NCBI_TaxID=216816;
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MEDLINE=22294977; PubMed=12381787;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B., Schell M.A., Karmirantzou M.-C., Desiere F., Bork P., Delley M., Pridmore R.D., Arigoni F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.1%; Score 76; DB 16; Length 699; 30.5%; Pred. No. 1e+02; tive 18; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 SSLGIPVNHLIEGS -----QKCVAELGPQAVGAVKALKALL 97
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SEQUENCE 699 AA; 70749 MW; 6523F9CA7E8BB943 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity 30.59
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Q8G4X4;
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Q8G4X4
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497 ABASKILYGEIPSIQKELAAAESADAESADASAANPAD--EPMVPDRVDADSVAEIVSDW 554
                                                                                                                                                                                                                         16 SSAAAFLVGSAKPVAQPVAALESA-AEAGAGTLANPLGTLNPL------KLLLSS 63
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"A sate of confered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                              18; Gaps
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STRAIN=A3(2) / M145;

MEDLINE=21996410; PubMed=12000953;

MEDLINE=21996410; PubMed=12000953;

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalo J., Hornsby T., Hornsby T.,

Rabbinowitsch B., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SC03765 OR SCH63:12C.
Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                       Length 889;
                                                                                       Query Match
15.1%; Score 76; DB 16; Length 889;
Best Local Similarity 25.7%; Pred. No. 1.3e+02;
Matches 26; Conservative 21; Mismatches 36; Indels
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Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oliver K., Harris D.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
Complete proteome. SEQUENCE 889 AA; 96313 MW; 704E8380EDA2A33C CRC64;
                                                                                                                                                                                                                                                                                                                                                           64 LGIPVNHLIEGSQKCVAE----LGPQAVGAVKALKALLGAL 100
                                                                                                                                                                                                                                                                                                                                                                                                         Ö9F216;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   459 AA
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MEDLINE=97000351; PubMed=8843436;
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Nature 417:141-147(2002).
BMBL; AL939117; CAC10303.1; -.
InterPro; IPR002550; CBS.
InterPro; IPR00644; CBS_domain.
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126 ETVGG 130
                                                                                                                     FROM N.A.
                                                      Aeropyrum pernix
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                                                                                                                        SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Q8XRM8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 -----LLSSLGI--PVNHLIEGSQKCVA----ELGPQAVGAVKALKALLGALTV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 TAASALVNELLSAQGVGNDASVIIEDAQGTVAAEHESNTPREPASTLKTLTALAASSTL 148
                                                                                                                                                                3 LAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLS 62
                                                                                                                                                                                      STRAIN=NCC 2705;
MEDLINE=2229.9977; PubMed=12381787;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
Pridmore R.D., Arigoni F.;
"The genome sequence of Bidiobacterium longum reflects its adaptation to the human gastrointestinal tract.";
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                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical secreted protein with D-Ala-D-Ala carboxypeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bifidobacterium longum.
Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
                                                                                                                                                                                                                                         62 GAQLGITUTSLVIGMLAEPSIAVLLRGPLTAMGLGGAASTVATLLGVV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 16; Length 496;
                                                                                                                                                                                                                          63 --SLGIPVNHLIEG--SQKCVAEL-GPQAV----GAVKALKALLGAL 100
                                                                                                            Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Carboxypeptidase; Complete proteome. SEQUENCE 496 AA; 50623 MW; 41572806ACD2D292 CRC64;
                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).
BMBL; AE014602. AANS2466.1;
GO; GO:0004185; F:serine carboxypeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000667; Peptidase S13.
Pfam; PF02113; Peptidase S13.
TIGREPAMS; TIGR00666; PBP4; 1.
                                                                        Complete proteome.
SEQUENCE 459 AA; 48880 MW; E96CE64003F45752 CRC64;
                                                                                                                                        12; Mismatches 49;
                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               544 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.0%; Score 75.5; Dilarity 30.3%; Pred. No. 78; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                          496 AA
                                                                                                            Query Match
15.0%; Score 75.5; I
Best Local Similarity 31.5%; Pred. No. 72;
Matches 34; Conservative 12; Mismatches
   InterPro; IPR005170; CorC_transpt-asc.
                                                                                                                                                                                                                                                                                                                          PRT;
               Pfam; PF00571; CBS; 2.
Pfam; PF03471; CorC HlyC; 1.
Pfam; PF01595; DUF21; 1.
SMART; SM00116; CBS; 1.
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hes 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=216816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                domain.
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Best Local Si
Matches 36,
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Q9YEG2
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Created)

O9YEG2; 01-NOV-1999 (TrEMBLrel. 12,

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72 -----LKVRFYSPGAPVESVVVLKPGEGVAARVELPEPAVEGVVDAMEGYDCSPVILGV 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 ALLGLCVALSCSSA-----AAFLVGSAKPVAQPVAA-----LESAAEAGAGTLANP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21681879; PubMed=11823852; Salanoubat M., Genin S., Arriguenave F., Gouzy J., Mangenot S., Salanoubat M., Genin S., Arriguenave F., Camus J.C., Catrolico L., Chandler M., Bilault A., Brottier P., Camus J.C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Felsenbach J., Boucher C.A.; Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
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Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 544;
                                                                                                                                                                                                                                                    Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales, Desulfurococcaceae, Aeropyrum.
NCBI_TaxID=56636;
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Last sequence update)
Last annotation update)
ol-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APE0614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UTM-2003 (TrEMBLrel. 24, Last annotation update)
Probable signal peptide protein.
RSP0803 OR RS01904.
Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 15.0%; Score 75.5; DB 17; Local Similarity 26.4%; Pred. No. 86; es 33; Conservative 19; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid megaplasmid.
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48 ANPLG---TENPLKLLLSSLGIPVNHLIEGSQKCVAEL---GPQAVGAVKALKALLG 98
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
NCBI_TaxID=1719;
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

Best Local Similarity 28.2%; Pred. No. 61;
Matches 29; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 AA
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                                                                          SEQUENCE FROM N.A.
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Q89H46
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                                                                                                                                                                                                           14 SCSSAAAFLVGSAKPVAQPVAALESAAEAGA----GTLANPLGTLNPLKLL---LSSLG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                      Gaps
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MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sagamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nitrogen-fixing symbiotic bacterium
                                                                                                                                                                      15;
                                                                                                                     Similarity 29.1%; Score 75.5; DB 16; Length 667; Similarity 29.1%; Pred. No. 1.18+02; 00; Conservative 14; Mismatches 44; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium pseudotuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.9%; Score 75; DB 16; Length 299; 25.5%; Pred. No. 50; tive 22; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Protecobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                           558 APVSQVVGSLITSPVGGGSVGVGQVGGAVSGAVAAGGSLLGSVS 600
                                                                                                                                                                                                                                                                                                    66 IPVNHL-----IEGSOKCVAELGPQAVGAVKALKALLGALT 101
           EMBL; AL646081; CAD17954.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
Plasmid; Complete proteome.
SEQUENCE 667 AA; 59635 MW; 7C78268AC33B9E2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 AA; 31937 MW; 86F2F929C7B18E94 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 IIGVVITALRPGGEKSFAELKPTILGLVAAAAFALSAV 174
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genomic sequence of nitroge Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197 (2002).
EMBL, APO05935, BAC45478.1; -GO, GO:0016020; C:membrane; IEA.
InterPro; IPRO0620; DUF6.
Pfam. PF00892; DUF6; 1.
Complete protecomes 299 Aa; 31937 MW; 86F2F9
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01-JUN-2003 (TrEMBLrel. 24, Le
01-OCT-2003 (TrEMBLrel. 25, Le
10-OCT-2003 (TrEMBLrel. 25, Le
BLI0213 protein.
Bradyrhizoblum japonicum.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                      30; Conservative
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Best Local Similarity 25.5
Matches 25; Conservative
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Best Local S
Matches 30
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FAGA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 ALSCSSAAAF-----LVGSAKPVAQPVAALESAAEAGAGTLANPLG-----TLNPLKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDLINE=22464998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
STRAIN-Wherten 1;
MIDLINE-1932508; PubMed=11934492;
MIDLINE-1932508; PubMed=11934492;
MIDLINE-1932508; PubMed=11934492;
MIDLINE-1932508; PubMed=11934492;
MIDLINE-1932508; PubMed=11934492;
MIDLINE-1932508; P.A., Songer J.G., Jost B.H.;
Midlington and role in virulence of putative iron acquisition genes from Corymbacerium pseudotuberculosis.";
FEMS Microbiol. Lett. 20841445 (2002).
EMBL; AF401634; AAL79811.1; -60, GO:0006810; F:transporter activity; IEA.
GO; GO:0006810; P:transporter activity; IEA.
HIGEPROS ; PROSOS PECCD; PECD.
PEAM; PF01032; PECCD; PECD.
PEAM; PF01035; AA, 36205 MW; F4DCF004C98CFCBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete' genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";

DNA Res. 9:189-197(2002)

EMBL, AP005957; BAC51414.1; -.

GO; GO:0016020; Cimembrane; IEA.

GO; GO:0005215; F:transporter activity; IBA.

GO; GO:0006810; P:transporter activity; IBA.

InterPro; IPR001851; Bac innem transp.

Pfam; PF02653; BPD_transp_2:.1.

Complete protecome.
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Best Local Similarity 28.2%; Pred. No. 63;
Matches 33; Conservative 17; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter permease protein.
BLR6149
                                                                                                                                                                                                                                                                                                                                                                                                                               14.9%; Score 75; DB 2; 28.2%; Pred. No. 61;
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Mol. Microbiol. 21:77-96(1996)
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                                                                                                                                                                                                                                    Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 27
Q9HNI9
ID Q9HNI9
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                                                                                                                                                                                                                                                                                                                               STRAIN.CSTBL/63; TISSUE=Lung;
MEDINE=22354681; PubMed=12466851;
The FANTOM Consortium Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length cDNAs.";
Nature 420:563-573(2002).
Nature 420:563-573(2002).
SEMBL; AR087322; BAC39845.1; -.
SEQUENCE 463 AA; 48966 MW; DA6327DB4AF27C78 CRC64;
   156 RQYRGVNETISSLLLVYIALAI-LNHLVEGIARDPASLNKPSTREIGAANMIGSIPG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
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MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered cogniss and a detailed genetic and physical map
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CT-2000 (TrEMBLrel. 24, Last annotation update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Putative membrane protein.
SCO4664 OR SCD40A.10C.
SCreptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCGI TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.9%; Score 75; DB 11; Length 463; 34.2%; Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Mismatches 30; Indels
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STRAIN=A3(2);
Cumino A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRANT=31(2);
Seeger K.J.; Harris D.;
Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SNF1-like kinase (Fragment)
Mus musculus (Mouse)
                                                                                                                   463 AA
                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 -----GSQSATPVLQTQA 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 34.21
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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                                                                                                                    080313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stage-specific S antigen-like protein.
Leishmania infantum.
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H.,
Crohin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).

Mature A17:141-147(2002).

EMBL; AL939121; CAB81855.1; ---
GO; GO:0016020; G:membrane; IEA.

InterPro; IPR003838; DUF214.

Fran; PP02687; Ftsx; 2.

Complete protecome.

SEQUENCE 611 AA; 61744 MW; 8F959720773AEDF9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 41.9%; Pred. No. 1.3e+02;
Matches 26; Conservative 9; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LSSLGIPVNHLIEGSQKCVAELGPOAVG--AVKALKALLGALTV 102
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STRAIN=MHOW/FRI/92/LEW2385;
Garin Y.J.-F., Menceur P., Lorenzo F., Bui H., Fratlong
Blanche H., Dedet J.-P., Derouin F.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY255809; AAPA1105.1, "BMBL, AY25580C GRC64;
SEQUENCE 119 AA, 11523 MW; E32E2EC612D720EC GRC64;
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14.6%; Score 73.5; DB 5; Length 1
Best Local Similarity 28.8%; Pred. No. 26;
Matches 30; Conservative 16; Mismatches 33; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Meddlberg J.F., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Nead T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Dawgharth A., Scott J., Bearan M., Brinksc L., Daugharty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Nadupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Wanathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mather J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Mellan J., Chouri H., Gallyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Rembl. Assonial oneidensis...;
In Leechnol 20:118-113(2002).
EMBL; AE015513; AANS3752.1; -.
ROGO GO:0019028; C:viral capsid; IEA.
GO: GO:0019028; F:structural molecule activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 ILGVNSGASCGAAAALLFGVGAGFGD--YALQGSAFLGAMAASGLIFFVARAAGRISSTR 172
                                                                                                                                                                                                                                                                                                                                                                                                  6 LIGICVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGT-----LANPLGTLNPLK 58
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                                                                                                                                                                                                                                                                                                                            Gaps
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14.6%; Score 73.5; DB 16; Length 389;
Best Local Similarity 33.0%; Pred. No. 92;
Matches 29; Conservative 12; Mismatches 26; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                             DB 16; Length 358;
                                                                                                                                                                                                                                    ch 14.6%; Score 73.5; DB 16; Length 3: Similarity 26.5%; Pred. No. 84; 27; Conservative 19; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 LLLSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGAL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 LLMS--GVAIGYMLSAATSFLIFSSDSAEGSRSVLFWLLGSL 212
                                                                                                                                                                  358 AA; 37275 MW; 7F3AA9BF28EE2607 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389 AA; 41160 MW; 42413806B5706AEB CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Prophage MuSol, protein Gp32, putative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9GUB5; PRELIMINARY; PRT; Q9GUB5; (TrEMBLrel. 16, Created)
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MEDLINE=22297686; PupMed=12368813;
InterPro; IPR000522; FecD. Pfam; PF01032; PecCD; 1. ProDom; PD001557; FecCD; 1.
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                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                            Complete proteome.
SEQUENCE 358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 389 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-2004483; PubMed=11016950; MEDLINE-2004483; PubMed=11016950; MEDLINE-2004483; PubMed=11016950; MEDLINE-2004483; PubMed=11016950; MEDLINE-20050483; PubMed=1101696; Medline M., Sbrogna J., Swartzall S., Wair D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Kellons K., Cruz R., Danson M.J., Hough D.W., Dandocks D.G., Jablonski P.B., Krebs M.P., Angevine C.M., Dale H., Alam M., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Bhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; Promos sequence of Halobacterium species NRC-1 ", pasSarma S.; Promos Sequence of Medical M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 İTSİFĞVVPFVDVGQYYSFLAAHENP-SIPLAAVETLGIAFAĞTV---LGA--PLALTFG 136
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
Nakagawa S.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005279; BAB99019-1; --
EMBL; AP005279; C:membrane; IEA.
GO; GO:0006215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR001851; Bac_inmem_transp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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14.6%; Score 73.5; DB 17; Length 331;
Best Local Similarity 27.9%; Pred. No. 77;
Matches 29; Conservative 17; Mismatches 35; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
NCBI_TaxID=1718;
                                                                                                                                             Transport protein.

PHNE OR VNG2084G.

Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).

Archaea, Buryarchaeota, Halobacteria; Halobacteriales;

Halobacteriaceae, Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 SLG-----IPVNHLIEGSQKCVAELGPQAVGAVKALKALLGAL 100
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                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:AFP binding; IEA.
GO; GO:0005215; F:AFP binding; IEA.
GO; GO:0006810; F:transporter activity; IEA.
GO; GO:0006810; F:transport; IEA.
InterPro; IPR000515; BPD transp.
InterPro; IPR005479; CP856_L D2.
Pfam; PF00528; BPD_transp; I.
PR054TE; PS00867; CP8ASE_2; I.
COMplete Protecome.
SEQUENCE 331 AA; 36613 MW; SAC660A5C6EA0E4;
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Q8NQ28;
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Q8NQ28
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229

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55 NPL------KLLLSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALT 101
                                                                                     69 HPLGHGRELYFWSFIVALLVFALGAGVS-LYEGIHIIA---PEPVANVKVNYIVLGLSF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 ALSCSSAAAFLVGSAKPVAQPVAALESAAE-AGAGTLANPLGTLNPLKLL-----LS 62
13 AALAGNLAIALT-KFAAAFFTGSSAMLSEGV---HSLVDTGNGGLLLYGMHRAARPADRT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermithis.";
NAt. Biotechnol. 21:526-531(2003).
EMBL, AP055050; BAC75147.1; -.
InterPro. IPR000600; ROK.
Pfam; PF00480; ROK; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=2147403; PubMed=11572948;
MEDLINE=2147403; PubMed=11572948;
Shinose M., Takahashi Y., Harrikava H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hatcroi M.;
Genome sequence of an industrial migroorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces avermitilis.
Bacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycese.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.5%; Score 73; DB 16; Length 429; 30.8%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 SRFLPAVRRHATSYALRHPAERVSIDLGRLGPDAVTAGAAILPL 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        429 AA; 45476 MW; DA40D29C898B4FDB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRLL 8165;
MEDLINE=22608306; PubMed=12692562;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Putative ROK-family transcriptional regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
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                                                                                                                                                                                                                                                                                                                                        429 AA
                                                                                                                                                                                                                                                                                                                                                                                                Created)
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PA0747.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 30.8'
Watches 32, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome. SEQUENCE 429 AA;
                                                                                                                                                          102 VF 103
                                                                                                                                                                                                               125 LF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metabolites.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 SSAAAFLVGSAKPVAQPVAALE----SAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNHL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
Rancko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Kancko T., Nakamura Y., Sato I., Sakamabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome stutcture of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti."
                                                                                                                            Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Pyraloidea, Pyralidae, Gallerinae, Galleria.
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1 Similarity 32.6%; Pred. No. 3.9e+02;
29; Conservative 13; Mismatches 24; Indels 23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39; Indels
                                                                                                                                                                                                                                                                                            TISSUE-Posterior silk gland;
Zurovec M., Kodrik D., Yang C., Sehnal F.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AR055239; AAG10393.1; -.
NON TER 1468 AA, 122705 MW; 2DAS9E1181BB3DDF CRC64;
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SEQUENCE 317 AA; 34064 MW; 36E60C5E58C72A54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O98048; PRT; 317 AA. 098048; O1-OCT-2001 (TrEMBLrel. 18, Created) 01-OCT-2001 (TrEMBLrel. 18, Last sequence update) 01-UTM-2003 (TrEMBLrel. 24, Last annotation update) ML4980.
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EMBL, AP003005, BAB51423.1; -..
GO, GO:0016020; C:membrane, IEA.
GO, GO:0008324; F:cation transporter activity; IEA.
GO, GO:0008812; P:cation transport; IEA.
F:Cation transport; IEA.
F:Cation efflux.
Fight Folists; Cation efflux.
TIGRFAMS; TIGR01297; GDF; 1x.
     (TrEMBLrel. 16, Last sequence update) (TrEMBLrel. 22, Last annotation update)
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                                                                  Heavy-chain fibroin (Fragment).
                                                                                                                 Galleria mellonella (Wax moth)
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Best Local Similarity 31.1*
Marches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 7:331-338(2000).
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SEQUENCE FROM N.A.
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                01-MAR-2001
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 8
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293 SNLKEAIQADEISQPLIWAVVSIAMVPLLSGSVFCYQTQVLNLDPSVIGMSKVIGQLMLL 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, BT005916; AA064851.1; -..
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016521; P:hydrolase activity, hydrolyzing O-glycosyl
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR004124; BT1.
InterPro; IPR001424; BT1.
InterPro; IPR001987; Glyco_hydro_5.
Pfam; PR03092; BT1: 1.
TIGRFAMB; TIGR00788; Ebt; 1.
PROSITE; PS00659; GLYCOSYL_HYDROL_FS; 1.
                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 28.2%; Pred. No. 1.5e+02;
Matches 35; Conservative 16; Mismatches 49; Indels
                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 542 AA; 59479 MW; 839B45F3FDD261B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                      COMPLETE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 15692 / PAO1;

STRAIN=ATCC 15692 / PAO1;

STRAIN=ATCC 15692 / PAO1;

STORE C.K., Plam X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Plam X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., A Hickey M.J., Brinkman F.S.L., Hufnagle W.O. Kowalik D.J., Lagrou M., A Garber R.L., Goltry L., Tolentino B., Westbrock-Wadman S., Yuan Y., Brody U.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

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IL Mature 406:959-964(2000).

BIRJ, PSES33; F83553;

RO, GO:0016491; F:oxidoreductase activity; IBA.

GO, GO:0016491; F:oxidoreductase activity; IBA.

GO, GO:0016491; F:oxidoreductase activity; IBA.

RO, GO:0016491; F:oxidoreductase activity; IBA.

RO, GO:0008152; P:mecabolism; IEA.

RO, GO:0008152; P:mecabolism; IBA.

RO, GO:0008152; P:mecabolism; IBA.

RO, GO:0008162; P:mecabolism; IBA.

RODE FROM III aldedh; 1.
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"Arabidopsis ORF clones.";
"Arabidopsis ORF clones.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR.2003 (TEMBLrel. 23, Created)
01-MAR.2003 (TEMBLrel. 23, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
ATIGA570/TIG11 17.
ATIGA570/TIG11 17.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicocyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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STRAINS-CV. Columbia.
STRAINS-CV. Columbia.
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima, M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashiizaki Y., Shinozaki K.,
"Arabidopsis thaliana Hall-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
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             Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
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Best Local Similarity 29.1%; Pred. No. 1.3e+02;
Matches 32; Conservative 13; Mismatches 41; Indels 2
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                                    Pseudomonadaceae; Pseudomonas
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                                                               NCBI_TaxID=287;
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Q8GYA1
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CONTRIBUTE FROM N.A.

STAIN=ATCC 1908 / CB15;

XI MEDLINE=21173698; PubMed=11259647;

XI MIGHTMAN W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

XI Mierman W.C., Feldblyum T.V., Laub M.T., Phadkock J.R.,

XI BOTOKRA I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

XI DOTOKRA I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

XI Colonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

XI Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

XI Complete genome sequence of Caulobacter crescentus.",

XI Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

XI EMBL, SABO5725; AAX22518.1;

XI MEROPS, T.D., 001;

XI MEROPS, T.D., 001;

XI MEROPS, T.D., 001;

XI MEROPS, T.D., 001;
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Caulobacter crescentus.
Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0003840; F:gamma-glutamyltransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR001011; Peptidase_II.
PRINTS; PR01210 GGTRANSFTASE.
TIGRRANS; TGR00066; g_glut_trans; I.
TTARRAPS, TGR00066; g_glut_trans; I.
Transferase; Complete protecome.
SEQUENCE 584 AA; 61016 MW; 5C3DA03B02261E75 CRC64;
                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
584 AA.
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Best Local Similarity 28.6%
Matches 28; Conservative
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2 KLAALLGLCVALSCSSAAAFLVGSAKPVAQPV--AALESAAEAGAGTLANPLGTLNPLKL 59

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DXS OR BP2798.
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A REDLINE=22227954; PubMed=12210271;
A Harris D.E., Holden M.TG., Churcher C.M., Bentley S.D., Mungall K.L.,
A Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
A chtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
A chtman M., Atkin R., Dawer S., Basham D., Bason N., Cherevach I.,
A chtman M., Atkin R., Dawer S., Basham D., Bason N., Cherevach I.,
A chtman M., Atkin R., Galis M., Cronin A., Doggett J.,
Beltwell T., Goble A., Hamlin M., Choil S., Ormond D., Price C.,
Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
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Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,
Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
Comparative analysis of the genome sequences of Bordetella pertussis,
Bordetella parapertussis and Bordetella bronchiseptica.";
BMEL, BK640442; CAE324091; -.
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12 ALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNHL
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31.1%; Pred. No. 1.7e+02;
iive 11; Mismatches 31; Indels 20;
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Alcaligenaceae; Bordetella.
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STRAIB12822 / ATCC BAA-587;
MEDLINE-22827954; Pubmed=12910271;
Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
                                                                                60 LLSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALL 97
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01-0CT-2003 (TEWBLrel. 25, Created)
01-0CT-2003 (TEWBLrel. 25, Last sequence
01-0CT-2003 (TEWBLrel. 25, Last annotati
1-deoxy-D-xylulose 5-phosphate synthase.
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DXS OR BPP2464.
Bordetella parapertussis.
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STRAIN=Tohama I.A. ATCC BAA-589 / NCTC 13251;

XX MEDLINE=Z2827954; PubMed=12910271;

XMEDLINE=Z2827954; PubMed=Z392964;

XMEDLINE=Z392964; PubMed=Z392964;

XMEDLINE=Z392964; PubMed=Z392964;

XMEDLINE=Z392964; PubMed=Z3929664;

XMEDLINE=Z3929646;

XMEDLINE=Z2827954;

XMEDLINE=Z28279696;

XMEDLINE=Z8282796;

XMEDLINE=Z82
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Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L., Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A., Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., Chillingworth T., Collins M., Cronin A., Dayis P., Dogget J., Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Unwin L., Whitehead S., Barrell B.G., Maskell D.J.; "Comparative analysis of the genome sequences of Bordetella pertussis, Nat. Genet. 35:32-40(2003).

PMBL, SK640403, CAE37759.1; -.
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Alcaligenaceae; Bordetella.
NCBL_TaxID=520;
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Local Similarity 31.1%; Pred. No. 1.7e+02;
hes 28; Conservative 11; Mismatches 31; Indels 3
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase.
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Matches 28; Conservative 11; Mismatches 31;
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EMBL; BX640419; CAE43071.1; -. Complete proteome.
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Matches 35; Conservative
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Job time : 43 secs
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                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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EMBL; AL022018; CAA17685.2; -.
PIR; T13613; T13613; EG:8D8.2; F1yBase; FBM0024366; EG:8D8.2.
SEQUENCE 1279 AA; 139070 MW; FA96DBBA48C5D5E9 CRC64;
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                               O46099,
01-JUN-1998 (TrEMBLrel. 06, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
EG:8D8.2 protein
EG:8D8.2 OR CG11409.
589 DHGDQAALLAGLGLDAAGIERAIRARFGAL 618
                                                                                 PRT; 1279 AA
                                                                                 PRELIMINARY;
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65 PEPARQGVHNALENILNAPUVL-----VNDVLQGEGEKAVNTFGRFMVNSTVGLAGLID 117
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Knietsch A., Waschkowitz T., Bowien S., Henne A., Daniel R.;

Knietsch A., Waschkowitz T., Bowien S., Henne A., Daniel R.;

Knietsch A., Waschkowitz T., Bowien S., Henne A., Daniel R.;

Wetagenomes of Complex Microbial Consortia Derived from Different

Soils as Sources for Novel Genes Conferring Formation of Carbonyls

from Short-Chain Polyols on Escherichia coli.";

J. Mol. Microbiol. Biotech. 5:46-56(2003).

GO: GO:0046821; C:extrachromosomal DNA; IEA.

InterPro; IPR00437; Prok lipoprot_S.
                                                              26;
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Length 1279;
Query Match
14.5%; Score 73; DB 5; Length 1279
Best Local Similarity 31.6%; Pred. No. 3.7e+02;
Matches 31; Conservative 12; Mismatches 29; Indels
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PRIMTS; PRO1063; VACJLIPOPROT.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1,
Lipoprotein; Plasmid.
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Plasmid pAK211.
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us-09-997-428-408.rpr

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probable transport
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1 MKLAALLGLCVALSCSSAAA......QAVGAVKALKALLGALTVFG 104
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Copyright (c) 1993 - 2004 Compugen Ltd.
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thromboxane A2 re FREAC-4 - human		N 101 10	ա տ		ب ف ف	610	
zein protein - me hypothetical prot		0,00	00 4**		66.		
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hypothetical protoconserved hypothe		10101	1 /O 44 C		, ששי	100 to 1	
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probable glycopro		100	a on m		67	. 4. 4. . 60 Q	
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hypothetical prot probable conserve		0 0 0	\sim 0 $^{\circ}$	 m m r	67. 7.57.	4 4 4 W 4 1	
hypothetical prot branched-chain ar		0 0	38	ო ო	φ.	4 4 L 2	
ferric enterobact ferric enterobact		0 0	നന	ო ო	68 68 68	€ 4 € 0	
P-glycoprotein - ferric enterobact		0.0	n n	m m	. w	3.7	
hypothetical prot ferric enterobact		0 0	33	. m	68.5 68.5	9 9 9	
probable ATP-depe probable ATP-depe probable adhesin		4 (4 (4	ง เก ด	m	φφσ	3 B B	
probable L-serine hypothetical prot		01 01 0	In In a	m m	69.5 69	300	

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probable anthranilate phosphoribotransferase - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000 C;Accession: T36304 R;Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill; J.; Barrell, B.G.; Rajandream, M.A submitted to the BMBL Data Library, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cjacession: AD2973
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dupont
C;Accession: T35054
R;Seeger, K.J; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A;Reference number: Z2156
A;Recession: T35054
A;Accession: T35054
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Recule type: DNA
A;Reciule type: DNA
A;Residues: 1-601 <SEE>
A;Cross-references: EMBL:AL031371; PIDN:CAA20556.1; GSPDB:GN00070; SCOEDB:SC4G2.19
A;Experimental source: strain A3(2)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-335 <SAU>
A;Cross-references: EMBL:AL035654; PIDN:CAB38583.1; GSPDB:GN00070; SCOEDB:SCE8.05c
A;Experimental source: strain A3(2)
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426 LVALLVTAVAGSGAATPALAVGAVAWAPLAAHTSSLLRQERATLHITATKGLGAGPVHLL 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 RHELLPAVVPPVLRHALLRLPGVALALASLGFLGLGAQPPSPEWGLLLAENQPYAERAPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- OPVAALESAAEAGAG----
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Agene: trp2; SCOEDB:SCE8.05c
C.Superfamily: anthranilate phosphoribosyltransferase; trpD homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 601;
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Best Local Similarity 34.5%; Pred. No. 8.2;
Matches 30; Conservative 9; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: T36304
A; Status: preliminary; translated from GB/EMBL/DDBJ.
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
15.4%; Score 77.5; D
Best Local Similarity 30.7%; Pred. No. 13;
Matches 42; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LAALLGLCVALSCSSAAAFLVGSA--KPVA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 AVGAVKALKALLGALTV 102
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                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: SCOEDB: SC4G2.19
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R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.)
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.)
R;Beference number: 216897
A;Reference number: 216897
A;Rocession: T09931
A;Molecule type: DNA
A;Residues: I-96 <BEV>
A;Coss.references: EMBL:AL079344; GSPDB:GN00062; ATSP:T1614.190
A;Experimental source: cultivar Columbia; BAC clone T1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nypotherical protein - common roundworm retrotransposon R4 (fragment)
C;Species: Ascaris lumbricoides (common roundworm)
C;Species: Ascaris lumbricoides (common roundworm)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C;Accession: 860004
R;Burke, W.D.; Mueller, F.; Bickbush, T.H.
Nucleic Acids Res. 23, 4628-4634, 1995
Nucleic Acids Res. 23, 4628-4634, 1995
A;Accession: 860004
A;Attle: R4, a non-IRR retrotransposon specific to the large subunit rRNA genes of 1A;Accession: 860004
A;Accession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ų,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
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C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 VALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGT------LANPLG-----
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C;Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase 4
C;Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Indels 27;
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Best Local Similarity 41.3%; Pred. No. 5.2;
Matches 26; Conservative 14; Mismatches 17; Indels
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.larity 27.8%; Pred. No. 20;
Conservative 15; Mismatches 23;
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                ALIGNMENTS
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A;Genome: retrotransposon
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Matches 25; Conserva
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T35054
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hypochetical protein APE0614 - Aeropyrum pernix (strain Kl)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: H72647
S;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerop; A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Helicobacter felis
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 08-Sep-2000
C;Accession: T47269
K;Bayle, D.; Wangler, S.; Weitzenegger, T.; Steinhilber, W.; Volz, J.; Przybylski, M.;
J. Bacteriol. 180, 317-329, 1998
A;Title: Properties of the P-type ATPases encoded by the copAP operons of Helicobacter
A;Reference mumber: 224437; MUID:98101471; PMID:9440521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: binds copper specifically [validated, MUID:98101471]
A;Note: involved in copper resistence
C;Superfamily: Entercoccus copper-transporting ATPase copA; ATPase nucleotide-binding C;Keywords: copper binding; hydrolase
F;8-37/Domain: heavy-metal-associated homology <HMA>
F;8-37/Domain: ATPase nucleotide-binding domain homology <ATN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     copper-transporting ATPase (EC 3.6.1.-) P-type copA [validated] - Helicobacter felis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: T47869
A;Accession: T47869
A;Actus: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rosidutes: 1-732 < RBAY
A;Crose-references: EMBL:AJ001932; NID:G2660538; PIDN:CAA05104.1; PID:G2660542
A;Experimental source: strain ATCC 49179
C;Genetics: A;Gene: CopA
C;Function:
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                           A, Residues: 1-699 <STO>
A, Croser references: GB:AE005673; NID:g13421344; PIDN:AAK22204.1; GSPDB:GN00148
C;Genetics:
A, Gene: CC0217
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                                                                                                                                                                                                                                                                                    3 LAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKL-LL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LIGICVALSCSSAAAFLVGSAKPVAQPVAAL----ESAAEAGAG---
                                                                                                                                                                                                                                                                                                                                                                                                           62 SSLGIPVNHLIEGS------QKCVAELGPQAVGAVKALKALL
                                                                                                                                                                                                                            37;
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                                                                                                                                                                 15.1%; Score 76; DB 30.5%; Pred. No. 21; tive 18; Mismatches
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                                                                                                                                                                                                   Best Local Similarity 30.5%
Matches 32; Conservative
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A; Molecule type: DNA
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Ca. ppr-2001
Hsg275
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Jabb, M.T.; DeBoy, R.T.; Dodson, K.J.; Dukkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
N, J; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable ABC transporter permease protein MJ0087 AGR_L_2865 [imported] - Agrobacterium to Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Date: 22-Oct-2001 #sequence_revision 25-Oct-2001 #text_change 18-Nov-2002
C;Date: 23-2328, 2333-2328, 2001
A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 233-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUD:21608551; PMID:11743194
A;Accession: G88309
A;Accession: G88309
A;Status: preliminary
A;Molecule type: DNA
         ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; WUID:21608550; PMID:11743193
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                                                                                   A; Accession: AD2973
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-355 < KUR>
A; Coss-references: GB: AE008689; PIDN: AAL44202.1; PID: g17741781; GSPDB: GN00187
A; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GB:AE007870; PIDN:AAK90001.1; PID:g15159970; GSPDB:GN00170
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Best Local Similarity 23.3%; Pred. No. 11;
Matches 28; Conservative 22; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.1%; Score 76; DB 2; Best Local Similarity 23.3%; Pred. No. 11; Matches 28; Conservative 22; Mismatches 4
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A)Cross-references: GB:AE007870; I
C)Genetics: A;Gene: AGR L 2865
A;Gene: AGR L 2865
A;Map position: linear chromosome
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A;Status: preliminary
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A, Gene: Atu3389
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Length 502;

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41; Indels

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A;Status: preliminary

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A Molecule type: DNA A Read to the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the C
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                                                                                                                                                                                                                                                                                                                              14.5%; Score 73; DB 2
29.1%; Pred. No. 29;
tive 13; Mismatches
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Best Local Similarity 29.1%
Matches 32; Conservative
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C.Species: Halobacterium sp. NRC-1
C.Species: Halobacterium sp. NRC-1
C.Species: Halobacterium sp. NRC-1
C.Species: Halobacterium sp. NRC-1
C.Species: C.S.Peb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C.Spacession: C84538
R.Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. N.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A.Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A.Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A.Authors: Hou, S.; Muldipacterium species NRC-1.
A.Reference number: A84160; Muldipacterium species NRC-1.
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A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: P83553
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C.Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C.Accession: F83553
R.Stover, C.K.; Phan, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S., Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jature 406, 959-964, 2000
                                                                                          A;Cross-references: DDBJ;AP000060; NID:g5104188; PIDN:BAA79584.1; PID:d1043370; PID:g510
A;Experimental source: strain K1
C;Genetics:
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probable aldehyde dehydrogenase PA0747 [imported] - Fseudomonas aeruginosa (strain PAO1)
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 LGTLNPLKLLLSSLGIPVNHL1-----EGSQKCVAELGPQAVGAVKALK-----ALLGA 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 37;
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                                                                                                                                                                                                                                                                                                                                                    Length 544;
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                                                                                                                                                                                                                                                                                                                                                         ; Score 75.5; DB 2;
; Pred. No. 18;
19; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                         15.0%;
illarity 26.4%;
Conservative 1
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Best Local Similarity
Matches 29; Conserva
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Best Local Similarity
Matches 33; Conserv
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A Molecule type: DNA
A, Residues: 1-331 <STC
                                                                                                                                                                                                                                                                                     A, Gene: APE0614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: phnE
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Cispecies: Caulobacter crescentus
Cispecies: Caulobacter crescentus
Cispecies: Caulobacter crescentus
Cipates: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
Cipates: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Haft, D.H.; Kolo
B; Laub, M.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, M.T.; Haft, D.H.; Kolo
H, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11255647
A;Accession: B87315
A;Accession: B87315
A;Accession: preliminary
A;Accession: Lebel AsTO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein 8D8.2 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13613
R;Papagiannakis, G.; Spanos, L.; Cox, S.; Siden-Kiamos, I.; Louis, C.
R;Papagiannakis, G.; Spanos, L.; Cox, S.; Siden-Kiamos, I.; Louis, C.
R;Papagiannakis, G.; Spanos, L.; Cox, S.; Siden-Kiamos, I.; Louis, C.
R;Papagiannakis, G.; Spanos, L.; Cox, S.; Siden-Kiamos, I.; Louis, C.
A;Reference number: 217695
A;Reference number: 217695
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;References: EMBL:AL022018; NID:e1273253; PID:e1426350; PIDN:CAA17685.2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: AE005673; NID: 913421716; PIDN: AAX22518.1; GSPDB: GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLAALLGLCVALSCSSAAAFLVGSAKPVAQPV--AALESAAEAGAGTLANPLGTLNPLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
324 ISPQARQRVLRLIAEGKAEGAECLLDGSQ-CQVEGYPNGNWLGPTLFRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                    gamma-glutamyltransferase [imported] - Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRD------GGSAVDAAVAIQAVL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 LLSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 14.5%; Score 73; DB Local Similarity 28.6%; Pred. No. 34; les 28; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: gamma-glutamyltransferase
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C.Species: Agrobacterium tumefaciens (C.Species: 30-Sep-2001 #text_change 18-Nov-2002 (C.Species): P.Species: B.; Agrung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldma A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.Science 294, 2323-2328, 2001 #the Plant Pathogen and Biotechnology Agent Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Areference number: Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the Agrobacterium the
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A;Reaidues: 1-528 <COL>
A;Cross-references: GB:Z80225; GB:AL123456; NID:g3242265; PIDN:CAB02326.1; PID:e266414
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-397 <KUR>
A;Crose-references: GB:AE007869; PIDN:AAK88359.1; PID:g15157842; GSPDB:GN00169
C;Genetics:
                                                                                                                             18 AAAFLVGSAKPVAQPVAALE-SAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNHLIEGSQ 76
                                                                                                                                                                                              18 AAAFLVGSAKPVAQPVAALE-SAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNHLIEGSQ 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 AKALIKGYGAPVAEGVAILKVEEAEAAAKQIPGPLYV----KKSQIHAGG------RGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAG------TLANPLGTLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
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14.3%; Score 72; DB 2; Length 397;
Best Local Similarity 36.2%; Pred. No. 28;
Matches 29; Conservative 8; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
14.3%; Score 72; DB 2; Length 528;
Best Local Similarity 28.4%; Pred. No. 38;
Matches 29; Conservative 15; Mismatches 34; Indel8
                                             31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Gene: RGC_4780
A;Map position: circular chromosome
C;Superfamily: succinate-CoA ligase (ADP-forming) beta chain
Pred. No. 28;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |||| | |: |::
58 K-FKELGPDAKGGVRLAKSI 76
                                                                                                                                                                                                                                                                                                                           77 KCVAELGPQAVGAVKALKAL 96
                                                                                                                                                                                                                                                                                                                                                                                  | |||| | ||: |::
58 K-FKELGPDAKGGVRLAKSI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 KCVAELGPOAVGAVKALKAL 96
Larity 36.2%;
Conservative
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: Rv2672
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C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession. AE2900
R;Wood, D.W.; Ascubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, K.; Romero, P.; Zhang, S.
Cience 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Bter, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AE2577; MUID:21608550; PMID:11743193
A;Accession: AE2900
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-397 <a href="https://www.main.com/">www.main.com/">www.main.com/main.com/main.com/</a>
A;Residues: 1-397 <a href="https://www.main.com/">www.main.com/www.main.com/</a>
A;Residues: 1-397 <a href="https://www.main.com/">www.main.com/www.main.com/</a>
A;Residues: 1-397 <a href="https://www.main.com/">www.main.com/www.main.com/</a>
A;Residues: 1-397 <a href="https://www.main.com/">www.main.com/www.main.com/www.main.com/</a>
A;Residues: 1-397 <a href="https://www.main.com/">www.main.com/www.main.com/</a>
A;Residues: 1-397 <a href="https://www.main.com/">www.main.com/</a>
A;Residues: 1-397 <a href="https://www.main
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amastigote-specific protein A2 precursor - Leishmania donovani infantum C;8pecies: Leishmania donovani infantum C;8pecies: Leishmania donovani infantum C;8pecies: 28-Apr-1995 #text_change 24-Nov-1999 C;Date: 28-Apr-1995 #text_change 24-Nov-1999 C;Accession: A56010 R;Charest, H;7 Matlashewski, G. R;Charest, H;7 Matlashewski, G. A;7tile: Developmental gene expression in Leishmania donovani: differential cloning and A;Reference number: A56010; MUID:94217695; PMID:7545921 A;Accession: A56010 A;Residues: 1-236 <CRANA A;Residues: 1-236 <CRANA A;Residues: 1-236 <CRANA A;Cross-references: GB:S69693; NID:9546453; PID:9546454 C;Superfamily: probline-rich protein C;Keywords: tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        succinyl-CoA synthetase beta chain [imported] - Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                                                                                           4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                                                                                                                                                                                       --AEAGAGTLANPLGTLNPLKLLLSSLGIPVN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLAALLGLCVALSCSSAAAFLVGSAKP--VAQPVAALESAAEAGAGTLANPLGTLNPLK 58
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                           56;
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                                                                                                                                            Query Match 14.5%; Score 73; DB 2; Length 1279; Best Local Similarity 31.6%; Pred. No. 75; Matches 31; Conservative 12; Mismatches 29; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 29.8%; Pred. No. 17;
Matches 31; Conservative 15; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.3%; Score 72; DB 2; Length 397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06 VGPQSVG-PLS------VGPQAVGPLSVGPQSVGPLSV
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C;Superfamily: succinate-CoA ligase (ADP-forming) beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 GKSDSAHKRYALDDYYPAESAPQPSVVAVADLRGLHGA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 HLIEGSOK-----CVAELGPQ-AVGAVKALKALLGA 99
                                                                                                                                                                                                                                                                                                                                          25 SAKPVAQPVAALESA-
          A;Introns: 65/2
A;Note: EG:8D8.2
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probable MFS transporter PA2214 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Species: Dece2000
C;Species: Dece2000
C;Accession: C8336
C;Accession: C8336
R;Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Badman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laxbig, K.; Lim Vature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path A;Reference number: A82950; MUD:20437337; PMID:10984043
A;Accession: C8336
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A;Acce
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A;Experimental source: strain PAO1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: F98216
A;Status: prellminary
A;Molecule type: DNA
A;Residues: 1-887 «KUR»
A;Cross-references: GB:AE007870; PIDN:AAK89256.1; PID:g15159084; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L 1346
A;Map position: linear chromosome
C;Superfamily: endopeptidase Clp ATP-binding chain
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499 AGELTYGIIPGLEKELAAAEARDSSGAGSMVQEVVTPDNIAHVVSRWTGIPVDKMLEGQR 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 AAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLSS-LGIPVNHLIEGSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 PLKLLLSSLGIPVNHLIEGSOKCVAELGPOAVGAVKALKA-LLGALTVFG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
14.2%; Score 71.5; DB 2; Length 887;
Best Local Similarity 26.1%; Pred. No. 71;
Matches 23; Conservative 23; Mismatches 37; Indels 5
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Best Local Similarity 32.7%; Pred. No. 39;
Matches 36; Conservative 7; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 KCVA----ELGPQAVGAVKALKALLGAL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 KCVA----ELGPQAVGAVKALKALLGAL 100
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: B87634
E;Accession: B87634
B; iaub, M.T.; Peldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. R;Nistran, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Gwinn, M.L.; Haft, D.H.; Kolon
D; Istrolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ster, E.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Accession: AC3070

A/Status: preliminary

A/Status: preliminary

A/Nolecule type: DNA

A/Residues: 1-874 < KUR>

A/COSS-references: GB:AE008689; PIDN:AA144977.1; PID:g17742634; GSPDB:GN00187

A/Experimental source: strain C58 (Dupont)
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A;Residues: 1-462 <STO>
A;Cross-references: GB:AE005673; NID:g13424766; PIDN:AAK25070.1; GSPDB:GN00148
                     11 VALSCSSAAAFLVGSAKPVAQPVAALESAAEAG----AGTLANPLGTLNPLKLLLSSLGI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9/
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14.2%; Score 71.5; DB 2; Length 87.
Best Local Similarity 26.1%; Pred. No. 70;
Matches 23; Conservative 23; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 PLKLLLSSLGIPVNHLIEGSOKCVAELGPQAVGAVKALKALL 97
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14.2%; Score 71.5; DE
Best Local Similarity 31.2%; Pred. No. 37;
Matches 30; Conservative 12; Mismatches
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C;Superfamily: microbial L-serine dehydratase
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Apporthetical protein [imported] - Arabidopsis thaliana
("Specias: Arabidopsis thaliana (mouse-ear cress)
[C;Specias: Arabidopsis thaliana (mouse-ear cress)
[C;Accession: C66178

R;Theologis, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marzial
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Attle Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: R86141; MUID:21016719; PMID:11130712
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NiAlternate names: protein T3A5.80
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Nebel-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
Cispecies: H. Mawes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.; Quetier, P.;
Riblocecker, H.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.; Quetier, P.;
Askeference number: 223024
Ascession: T46147
                                                                                                                                                             122 IGNILGGYLLLTTPPKISFLVFSALLSLQLVVSLSSKEESFGLPRIAETSSVLESVKKQI 181
                                                                                                              18 AAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTINPLKLLLSSLGIPVNHLIEGSQK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Molecule type: DNA
A; Molecules: 1-431 < STO>
A; Cross-references: GB: AE005172; NID: g2494120; PIDN: AAB80629.1; GSPDB: GN00141
C; Genetics:
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                                      5; Gaps
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                                  41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-452 <BLD.>
A;Cresivers-references: EMBL:AL132979
A;Experimental source: cultivar Columbia; BAC clone T3A5
Best Local Similarity 27.6%; Pred. No. 83; Matches 24; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                            78 CVAELG----PQAVGAVKALKALLGAL 100
                                                                                                                                                                                                                                                                                                                                                         524 RLISLADKLHERVVĠQDEÁVKÁVAAÁI 550
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A;Map position: 3
A;Introns: 44/1; 176/2; 243/1
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A;Map position: 1
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Superfamily: endopeptidase CLp ATP-binding chain.

Saverage: ATP, hydrolase; molecular chaperone; nucleotide binding; P-loop; Lato-245/Region: nucleotide-binding motif B (P-loop)

Saverage: ATP, Region: nucleotide-binding motif A (P-loop)

Saverage: ATP (Lys) #status predicted

Saverage: ATP (Lys) #status predicted
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 AAAFLVGSAKPVAQPVAALESAAEAGGTLANPLGTLNPLKLLLSSLGIPVNHLIEGSQK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable endopeptidase Clp ATP-binding chain - Arabidopsis thaliana N;Alternate names: ATP-dependent Clp proteinase regulatory chain N;Contains: adenosinetriphosphatase (BC 3.6.1.3) C;Gontains: adenosinetriphosphatase (BC 3.6.1.3) A;Variety: chruhdapsis thaliana (mouse-ear cress) A;Variety: columbia C;Date: 03-Aug-1998 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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14.0%; Score 70.5; DB 2; Length 668;
Best Local Similarity 27.6%; Pred. No. 66;
Matches 24; Conservative 17; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.0%; Score 70.5; DB 2; Length 831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Map position: 4
C,Superfamily: endopeptidase Clp ATP-binding chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 CVAELG----PQAVGAVKALKALLGAL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Map position: 4COP9-4G3845 Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Gene: dl3375w
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                                                                                     RESULT 22
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us-09-997-428-408.rpr

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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: C70582
C;Accession: C70582
R; Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R;Cole, S.T.; Brosch, R.; Perkhill, J.; Geneles, S.; Hamlin, N.; Holroyd, S; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seger, K.; Skelton, S.; Squares, S.
Nature 333, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MulD:98295987; PMID:9634230
A;Reference number: A70500; MulD:98295987; PMID:9634230
A;Reference number: A70500; MulD:98295987; PMID:9634230
A;Residues: 1-423 cCOL>
A;Cross-references: GB:295210; GB:AL123456; NID:g3261757; PIDN:CAB08513.1; PID:e315217, A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross references: GB;AE001948; GB:AE000513; NID:g6458680; PIDN:AAF10540.1; PID:g64586
A;Experimental source: strain R1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          띪
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: G75454
G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accession: G;Accessio
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C,Superfamily: Synechocystis hypothetical protein s1r1977
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                                                                                                                                                                                                                                                                                                                                                                    160 NTAVLAFGBAKQI--PVAILRVVSD----TMTQDLPDLNGVFTEQGALQPLPLAKALLRR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LAALLGLCVALSCSSAAAFLVGSAKPV-AQPVAALESAAEAGAGTLANPLGTLNPLKLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 LAGSAĞWPGAAAQSAPAVRILFSARSVPALPVNALPAAPAPAPGLPASILSSLSSLNI--
                                                                                                                                                                                                                                                                                                    17 SAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPL------GTLNPLKLLLSSLGI
                                                                                                                                                                                                                  25;
                                                                                                                               DB 2; Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----IPI-----GSERLEVLGVAPDALAGTPGNPQGALLAVRGVGG 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33; Indels
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 PV--NHLIEGSOKCVAELGPQAVGAVKALKALLGAL 100
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Pred. No. 48;
18; Mismatches
                                                                                                                           Query Match
Best Local Similarity 31.2%; Pred. No. 30;
Matches 30; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 32.1%;
Matches 34; Conservative 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: G75454
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-396 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 1
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Residues: 1-244 <KAN>
Cross-references: EMBL:D90912; GB:AB001339; NID:g1653228; PIDN:BAA18214.1; PID:g165329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;FXCETUS: DIRELIMINARY
A;MOLECULE type: DNA
A;Residuss: 1477 <HEX
A;CCOSA-references: GB:AE004237; GB:AE003852; NID:g9656107; PIDN:AAF94751.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: 875653
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O; K.; Owkmura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA, Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable multidrug transporter VC1597 [imported] - Vibrio cholerae (strain N16961 serogi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Riffeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                           'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388 AN-LGRITAMASLSRSLGASVGTAFFGTLIYSLLFGLSPNSGLQALAAL-PQSEILHAFQ 445
                                                                                                                                                                                                                                                                                                                           48 ANPLGTINPLKILLSSLGIPVNHLIEGS-------86
                                                                                                                                                                                                                                                                        9 LCVALSCSSAAAFLVGS----AKPVAQPVAALESAAEAGA----GTLANPLGTLNPLKLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 06-Jan-2003
C;Accession: D82179
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                                                                                                                                                                                           37; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein slr1977 - Synechocystis sp. (strain PCC 6803)
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Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 477;
                                                                                                    Query Match
13.9%; Score 70; DB 2; Length 452;
Best Local Similarity 26.9%; Pred. No. 50;
Matches 28; Conservative 21; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LSSLGIPVNHLIEGSOKCVAELGPQAVGAVKALKALLGALTVFG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 VSSTSTSIDAIVPHGLGLGLPCGGESSSGLKEL--MMGNSSVFG 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTL-
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13.9%; Score 70; DB
Best Local Similarity 28.1%; Pred. No. 53;
Matches 38; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 1
C;Superfamily: multidrug-efflux transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 VG-AVKALKALLGAL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| || || || ||||||
IGFAVAALLALLGAL 460
                               A, Note: T3A5.80
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probable ATP-dependent proteinase ATP-binding chain - Streptomyces coelicolor (fragmen C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor (jace: 03-bec-1999 #text_change 02-Feb-2001 C;Accession: T36551 B;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. #theference number: Z21609 #A;Reference number: Z21609 #A;Accession: T36551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: D75393
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-627 <WHI>
A;Resicues: CETECENCES: GB:AE001990; GB:AE000513; NID:G6459214; PIDN:AAF11026.1; PID:G6459
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1.853 <MUR>
A;Cross-references: EMBL:LL049754; PIDN:CAB42048.1; GSPDB:GN00070; SCOEDB:SCH10.39c
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54
                                                64
                                                                                           2 LAGLLAACNSTESALDIQGSNKDTGQ--AATTAPSNAPVATPAPQRATLKPGKLHIAPIV 59
                                                                                                                                                                                                                                                                                                                         serine proteinase, subtilase family - Deinococcus radiodurans (strain R1)
C,Species: Deinococcus radiodurans
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 KLILLGAALALSGASGAS--AGSLSP----TLLQKARAGDQT---PIGVIVRFNVAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLL
                                             6 ILIGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLSSL-
Gaps
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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C;Superfamily: endopeptidase Clp ATP-binding chain
C;Superfamily: endopeptidase Clp ATP-binding chain
C;Scywords: ATP; molecular chaperone; nucleotide binding; P-loop
F;195-202/Region: nucleotide-binding motif A (P-loop)
F;597-604/Region: nucleotide-binding motif B (P-loop)
F;65-670/Region: nucleotide-binding motif B F;601/Binding site: ATP (Lys) #status predicted
F;603/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.7%; Score 69; DB 2; Length 627; 31.1%; Pred. No. 86; ive 14; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 853;
                                                                                                                                                                                  60 GAPVNVVTPLTHRMNDDAKAMGIELAGNNDPSAAVVIKGYFSVL 103
Indels
                                                                                                                                                    65 GIPVN-----HLIEGSOKCVA-ELG----POAVGAVKALKALL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 SSLGIPVNHLIEGS-OKCVAELGP-----OAVGAVKALKALL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45;
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 69;
     14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 31.1%
Matches 32; Conservative
     31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Map position: 1
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Gene: DR1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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        Matches
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C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AD0782
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R; Pickard, D.; Wain, J.; Churcher, th, T; Connerton, P; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S; Noule, S.; Moule, S.; O'Gacra, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Atcession: AD0782
A;Feference number: AB0502; MUID:21534947; PMID:11677608
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Residues: 1455 cPAR>
A;Construction of BRAINS (BBNC) PIDN:CAD02578.1; PID:g16503436; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: microbial L-serine dehydratase
C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
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A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 SAASALPPFTPPVQGTGPAGPAAAAAATQAAGAGAVADAQATLAQLPPGILSDILSALA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 AALLGL---C---VALSCSSAA---AFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTL 54
                                                                                                            16 SSAAAFLVGSAKPV----AQPVAALESAAEAGAGTLANPLGTL-----NPLKLILLSSLG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                           Gaps
                                                           11;
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13.8%; Score 69.5; DB 2; Length 455;
Best Local Similarity 29.0%; Pred. No. 56;
Matches 31; Conservative 17; Mismatches 26; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 NPLKLLLSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 423;
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     Query Match
Best Local Similarity 31.8%; Pred. No. 52;
Matches 28; Conservative 12; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 69; DB 2;
Pred. No. 23;
                                                                                                                                                                                                                                        : | | ; ; | | | ; ; ; 218 ANADPLITSGLLGIASTLNPQ-VGSAQPI 244
                                                                                                                                                                                                             66 IPVNHLIEGSQKCVAELGPQAVGAVKAL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.7%;
29.8%;
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-170 <KUR
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A,Residues: 1-1724 c.LEG>
A;Cross-references: EMBL:L29485; NID:g460312; PID:g460313; PIDN:AAA65541.1
C,Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette
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                             104
                                                                             131 LTLAWPLGAVGAALVLTA------GSWRLLARIRPTDTRAV----GVAGVLAVFG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68
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C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 SAKPVAQPVAA---LESAAEAGAG--TLANPLGTLNP-------LKLLLSSLGI
                         GTLANPLGTLNPLKLLLSSLGI PVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---VAALESAAEAGAGTLANPL------GTLNPLKLLLSSLGIPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 NHLIEGSQKCVAELGPQA------VGAVKALKALLGALTVFG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1724;
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R;Legare, D.; Hettema, E.; Ouellette, M.
Mol. Biochem. Parasitol. 68, 81-91, 1994
A;Title: The P-glycoprotein-related gene family in Leishmania.
A;Reference number: Z18879; MUID:95198776; PMID:7891750
A;Accession: T18343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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13.6%; Score 68.5; DB 2;
Best Local Similarity 29.2%; Pred. No. 2.7e+02;
Matches 28; Conservative 10; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Genetics:
A,Gene: STY0636
C,Superfamily: vitamin B12 transport protein btuC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.6%; Score 68.5; D
19.5%; Pred. No. 51;
tive 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LAALLGLCVALSCS-----SAAAFLVGSA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -glycoprotein - Sauroleishmania tarentolae
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Matches
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Cypothetical protein Wng1852h [imported] - Halobacterium sp. NRC-1
Cypothes: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
Cyfocession: F84346
Fy M.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld Jung, K.H.; Alam, M.; Freitas, S.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Yersinia peetis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AB0074
E;Parchibil, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rucharford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A;Molecule type: DNA
A;Residues: 1-277 <STO>
A;Cross-references: GB:AE004437; NID:g10581298; PIDN:AAG20058.1; GSPDB:GN00138
C;Genetics:
                                        4
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A,Residues: 1-3295 «KUR»
A,Cross-references: GB:AL590842; PIDN:CAC89456.1; PID:g15978692; GSPDB:GN00175
C;Genetics:
A,Gene: YP00599
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71 VAPVFGSPIVYATTAAAAGATWLAVRRFGARPQVLLAGVGAVAAAVPITAALARGWTAGT 130
                                                                                                                                           44
                                                                                               17 SAAAFLVGSAKPVAQPV-AALESAAEAGAGTLA-NPLGTLNPLKLLLSSLGIPVNHLIEG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 AALLGLC-----VALSCSSAAAFLVG-----SAKPVAQPVAALESAAEAGAGTLA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3007 GAAGAATAELMAPTIISALGWDKNTLTEGOKQAVSALSTLAAG-----LAGGLT 3055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----FLVG-SAKPVAQPV-AALESAAEAGA
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                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 13.6%; Score 68.5; DB 2; Length 277; I Similarity 27.5%; Pred. No. 42; 33; Conservative 14; Mismatches 40; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Indels
                                        Indels
   ; Pred. No. 1.2e+02;
21; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.7%; Score 69; DB 2; I
27.6%; Pred. No. 4.6e+02;
                                                                                                                                                                                                                                              75 -SQKCVA---ELGPQAVGAVKALKALLGAL 100
                                                                                                                                                                                                                                                                                   15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LAALLGLCVALSCSSAAA------
   27.8%;
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Best Local Similarity 27.65
Matches 32; Conservative
                                            25; Conservative
Best Local Similarity
Matches 25; Conserv
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Best Local Si
Matches 33;
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C;Accession: A85558
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May! Aller, L.; Accession: A85558
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May! Aller, L.; Accession: Assertion of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85558
A;Atatus: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Across-references: GB:AE005174; NID:g12513480; PIDN:AAG54925.1; GSPDB:GN00145; UWGP:Z
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. Dha, Res. 8, 11-22, 201.
DNA Res. 8, 11-22, 201.
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and ge A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ferric enterobactin (enterochelin) transport EC80629 [imported] - Escherichia coli
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-334 <HAY>
A;Cress-references: GB:BA000007; PIDN:BAB34052.1; PID:g13360087; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 LEAFSGICOSADCTIVLDARLPRILAGLIAGGALGLAGALMOTLIRNPLADPGLLGVNAG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 LEAFSGICOSADCTIVLDARLPRILAGLLAGGALGLAGALMQTLIRNPLADPGLLGVNAG 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C;Accession: E90707
Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 -----GTLNPLKLLLSSLABAGAGTLANPL-----GTLNPLKLLLSSLGIPV
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C;Superfamily: vitamin B12 transport protein btuC
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C,Superfamily: vitamin B12 transport protein btuC
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Pred. No.
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22.1%;
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Best Local Similarity 22.1
Matches 34; Conservative
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hes 34; Conservative
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A; Molecule type: DNA
A; Residues: 1-23,4L,,235-334 cCHE>
A; Cross-references: EMBL:X59402; NID:g41433; PIDN:CAA42043.1; PID:g41434
A; Cross-references: EMBL:X59402; NID:g41413; PIDN:CAA42043.1; PID:g41434
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
Science 277, Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Status; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Shea, C.M.; McIntosh, M.A.
Mol. Microbiol. 5, 115-1428 1991
A/Title: Mucleotide sequence and genetic organization of the ferric enterobactin transpo
A;Reference number: S16295; MUID:92157868; PMID:1838574
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A; Molecule type: DNA
A; Residues: 1-334 cSHE>
A; Residues: 1-334 cSHE>
A; Cosalcues: 1-334 cSHE>
A; Cosalcues: 1-334 cSHE>
A; Crosalcues: EMBL:X57471; NID:g41429; PIDN:CAA40707.1; PID:g41430
B; Chenault, S.S.; Barhart, C.F.
Mol. Microbiol: 5, 1405-1413; 1991
A; Title: Organization of genes encoding membrane proteins of the Escherichia coli ferrie
A; Reference number: S16305; MUID:92157867; PMID:1787794
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                                                                                                                                                                                                                      ferric enterobactin transport protein fepD - Escherichia coli (strain K-12) N.Alternate names: ferrienterobactin permease fepD C.Speciese: Escherichia coli C.Speciese: Escherichia coli C.Date: 04-Dec-1992 #sequence revision 04-Dec-1992 #text_change 01-Mar-2002 C.Accession: S16296; S16305; D64792; S14841
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73.5
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72
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Perfect score:
                                                                                                                                                                                                                     Scoring table:
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                                                                           OM protein
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                                                                                                                                                                                           Sequence:
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Result

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104 AA

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STANDARD;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                   Mus musculus
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               MOUSE
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Best Local
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096P<u>E</u>1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license@isp-sib.ch (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 WKIAALIGICVALSCSSARAFIVGSAKPVAQPVAALESAAEAGAGTLANPLGTINPLKIL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Companies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL
                                                                                                                                                                                                                                                                                                                 MEDINE=21396515; PubMed=11481438; Krop I.E., JeVangie R., Seth P., Krop I.E., Sgrol D., Porter D.A., Lunetta K.L., LeVangie R., Seth P., Kaelin C.M., Rhoi E., Bosenberg M., Schnitt S., Marks J.R., Pagon Z., Belina D., Razumovic J., Polyak K.; Schnitt S., Marks J.R., Pagon Z., Belina D., Razumovic J., Polyak K.; Pagon Z., Razumovic G., Polyak K.; Pagon Z., Polyak K.; Pagon D., Razumovic J., Polyak K.; Polyak K.; Pagon D., Razumovic J., Polyak K.; Pagon Z., Pagon D., Razumovic J., Polyak K.; Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., Pagon Z., P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
                                        Q96QRI; Q96PL0;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Utercolobin-related protein 2 precursor (cytokine HIN-1) (High in normal-1) (Secretoglobin family 3A member 1).
SCGSDA1 OR UGRP2 OR HIN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=21539178; PubMed=11682631;
Nilmi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
UTEROGLOBIN-RELATED PROTEIN 2.
R -> A (IN REF. 2).
1063873C8FAE6015 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 606500; -. C:extracellular; NAS. GO; GO:0005576; C:extracellular; NAS. GO; GO:0005125; F:cytokine activity; NAS. GO; GO:0030308; P:negative regulation of cell growth; NAS. GO; GO:0042127; P:regulation of cell proliferation; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
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                      104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AY040564; AAK82942.1; -. EMBL; AF313458; AAL26217.1; -.
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104 AA; 10185 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:18384; SCGB3A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity Artive Matches 103; Conservative
                      STANDARD;
                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytokine, Signal
                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kimura S.;
                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKL-AALLGLCVALSCSSAAAFLVGS-AKPVAQPVAALESAAEAGAGTLAN-PLGTLNPL
                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE-21396515; PubMed=11481438; Krop I.E., Levangie R., Seth P., Krop I.E., Sgroi D., Porter D.A., Lunetta K.L., Levangie R., Seth P., Kaelin C.M., Rhei E., Bosenberg M., Schnitt S., Marks J.R., Pagon Z., Belina D., Razumovic J., Polyak K.; "HIN-1, a putative cytokine highly expressed in normal but not cancerous mammary epithelial cells."; Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "UGRP1, a uteroglobin/clara cell secretory protein-related protein, a novel lung-enriched downstream target gene for the T/EBP/NKX2.1 homeodomain transcription factor."; Mol. Endocrinol. 15:2021-2036(2001).
1- FUNCTION: Potential growth inhibitory cytokine.
1- SUBCELLULAR LOCATION: Secreted (By similarity).
1- SUBCELLULAR LOCATION: Delongs to the uteroglobin family. UGRP subfamily.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2010 (Rel. 41, Last annotation update)
normal-1) (Secretoglobin family 3A member 1).
SCGB3A1 OR UGRP2 OR HIN1.
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uteroglobin-related protein 1 precursor (Secretoglobin family 3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-21539178; PubMed=11682631;
MINIM I., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
Ximira S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.8%; Score 250; DB 1; Length 104; 57.0%; Pred. No. 8.2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
UTEROGLOBIN-RELATED PROTEIN 2.
D62F0E601FB57A6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF313456, AAL26216.1; -. MGD, MGI:1915912; Scgb3a1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 104 AA; 10591 MW;
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                                                                                                                                                                                                                            (Mouse)
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SCGB3A2 OR UGRP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEEPSEE
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Compas 1500
            Sequence Companier
                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a lung specific gene (LSG) protein Lng107 from human clone ID 586271. The LSG has high level of tissue specificity for lungs and is overexpressed in cancerous tissues. The sequence serves as a diagnostic marker for detecting, monitoring, staging and prognosticating lung cancer. The diagnosis involves comparing levels of LSG in samples obtained from patient and normal control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MYLAALIGECVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKIL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirriosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's disease; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MXLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAABAGAGTLANPLGTLNPLKLL
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                                                                                                                                                                                                                                                                                                          A new method for diagnosing, monitoring and staging lung cancer,
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 502; DB 3;
100.0%; Pred. No. 1.4e-49;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                             Example 2; Page 38-39; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY87288 standard; protein; 104 AA.
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Best Local Similarity 100.
Matches 104; Conservative
                                                                                                                                                                                                                         Sun
                                                                                                                                                                                    (DIAD-) DIADEXUS LLC
                                                                                                                                                                                                                       Yang F, Macina RA,
                                                                                                                                                                                                                                                        WPI; 2000-116320/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 104 AA;
                                                                                                                                                                                                                                                                           N-PSDB; AAZ29723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-1998;
                                                 W09960160-A1.
                  Homo sapiens.
                                                                                                                                                     21-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-MAY-2000
                                                                                                                    12-MAY-1999;
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                                                                                  25-NOV-1999
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides membrane-bound PRO polypeptides and polymucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE idends and various enzymes. The membrane-bound proteins and receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be receptor-ligand interactions. The membrane-bound proteins can also be semployed for screening of potteins peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hypridization probes, in chromsome and gene mapping and in the generation of antisense RNA and DNA. PRO mucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by IS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Specific Gene; LSG; Lng107; human; diagnostic marker; prognosticate; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLAALIGICVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLAALIGICVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                Watanabe CK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 104;
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                                                                                                                                                                                                                                                                                                                                                                 Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 502; DB 3;
Pred. No. 1.4e-48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Fig 290; 822pp; English.
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9805-0097141P-
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Best Local Similarity
Matches 104; Conserv
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Yuan J;
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26-AUG-1998;
26-AUG-1998;
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26-AUG-1998;
31-AUG-1998;
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Wood WI,
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26-AUG-19
26-AUG-19
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human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anticinationobial, mootropic, hepatotropic, neuroprotective, cardiovascular and antisthmatic activities, and can be used in gene therapy. HSPPs can a associated with decreased activity or function of HSPP. Antagonists of associated with decreased activity or function of HSPP. Antagonists of in the prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (including anametion, cardiovascular, neurological, inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anamemia, aschaemic heart disease, Alzheimer's, Parkinson's or Huttington's ischaemic chart disease, Alzheimer's, Parkinson's or Huttington's ischaemic heart disease, Alzheimer's, Parkinson's or Huttington's diseases, schizophrenia, ovulatory defects, muscular dystrophy, HSPP curdecting HSPP in standard hybridisation and amplification assays (for detecting HSPP are also used to raise specific antibodise (Ab) and to screen for agonists and antibodise (Ab) and to screen for agonists and antibodise (Ab) and to screen for agonists and antibodise (Ab) and to screen for agonists and antagonists, in competitive diseases (in usual immunoassays), as therapeutic antagonists, in competitive drug screens, and for purification of HSPP from natural conversed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLAALIGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLAALLGLCVALSCSSAAAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLL 60
                                                                                                                                                                                                                                                                   New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, secreted and transmembrane protein; PRO; cytostatic, cell death, cancer; chromosomal mapping; gene mapping; tissue typing;
                                                                                                                          Corley NC, Guegler KJ, Baughn MR;
H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 502; DB 3;
100.0%; Pred. No. 1.4e-48;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 206; 327pp; English.
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Yue
98US-0102686P.
98US-0102686P.
98US-0112129P.
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Akerblom IE, Au-Young J,
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Matches 104; Conservative
                                                                                    (INCY-) INCYTE PHARM INC
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N-PSDB; AAZ98173.
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  31-JUL-1998;
01-OCT-1998;
11-DEC-1998;
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                                                                                                                                                                      Bandman 0;
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The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bloactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and game mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide cancer. Anti-PRO antibodies can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44650 to AAF44650 to AAF44650 to AAF44650 to AAF44650 to AAF44650 to AAF44650 to AAF44650 to AAF44650 to AAF44650 to AAF44650 to AAF44650 to AAF4650 to AAF46650 to AAF4650 to AAF4660 to AAF4650 to AA
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Godowski PJ;
Paoni NF;
Wood WI;
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99US-014475BP.
99US-0145698P.
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99US-0149396P.
99WO-US021090.
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2000WO-US000376
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N-PSDB; AAF44249.
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Ferrara N, Fong S,
Grimaldi CJ, Gurney
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11-FEB-2000; 2
18-FEB-2000; 2
22-FEB-2000; 2
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02-MAR-2000; 2
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05-JAN-2000;
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Zhang Z;
Companison
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Indels

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100.0%; Score 502; DB 4; 100.0%; Pred. No. 1.4e-48; 0; Mismatches

Query Match Best Local Similarity 100. Matches 104; Conservative

1 MKLAALLIGLCVALSCSSAAAFLVGSAKPVAQPVAALBSAAEAGAGTLANPLGTLNPLKLL

us-09-997-428-408.rag

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1 MKLAALLGLCVALSCSSAAA......QAVGAVKALKALLGALTVFG 104
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Abb6580 H
Abus9173 N
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96US - 0095282P.
96US - 00953304P.
96US - 0095318P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0096146P.
98US-0096757P.
98US-0096766P.
98US-0096768P.
98US-009673P.
98US-009689P.
98US-009689P.
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98US-0095929P.
98US-0096012P.
98US-0096143P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0091360P
                                                                                                SEGUENCE COMPARISON
Abo06270 Novel hum
Abr59306 Human sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                de, PRO polypeptide, LDL receptor, TIE ligand, immunoadhesin, gene mapping.
      ABC06270
ABRS9306
                                                                                                                                                                                                                                                             AAY66757 standard; protein; 104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Membrane-bound protein PRO1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0087607P

98US-0087603P

98US-0088021P

98US-0088021P

98US-0088023P

98US-0088028P

98US-0089028P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US012252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Membrane-bound polypeptide;
pharmaceutical; receptor imm
                                                                                                                                                                                                                                                                                                                                                                             05-APR-2000 (first entry)
            93
         \frac{31.9}{31.9}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W099630'88-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUN-1999;
         160
                                                                                                                                                                                                                                                                                                                      AAY66757;
                                                                                                                                                                                                    RESULT 1

AAY66757

AAY6757

AAY67

AAY
      100
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